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4 102 3 US-08-639-075A-125 Sequence 125, App 4 102 3 US-09-012-631-125 Sequence 125, App 4 102 3 US-09-012-692-125 Sequence 125, App 4 102 3 US-09-012-692-125 Sequence 125, App 5 Sequence 125, App 6 1 US-08-485-455-75 Sequence 75, Appl 6 2 US-08-484-211C-75 Sequence 75, Appl 6 3 US-08-906-616-75 Sequence 75, Appl 6 4 3 US-08-906-616-75 Sequence 75, Appl 7 6 4 3 US-08-906-616-75 Sequence 75, Appl 8 6 3 US-08-906-616-75 Sequence 75, Appl 9 6 4 3 US-08-917-795-75 Sequence 75, Appl 9 6 4 3 US-08-917-795-75 Sequence 75, Appl 9 6 4 3 US-08-817-795-75 Sequence 75, Appl 9 6 6 3 US-08-618-75 Sequence 75, Appl 9 6 9 US-08-618-75 Sequence 75, Appl 9 6 9 US-08-618-75 Sequence 75, Appl 9 6 9 US-08-618-75 Sequence 75, Appl	RESULT 1 US-09-949-016-8151 Sequence 8151, Application US/09949016 Sequence 8151, Application US/09949016 PRECAL INFORMATION: APPLICANT: VENTER, J. Craig et al. TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED TITLE OF INVENTION: POLYMORPER: US/09/949,016 CURRENT FILING DATE: 2000-04-14 PRIOR APPLICATION NUMBER: 60/231,768 PRIOR PLING DATE: 2000-10-20 PRIOR FILING DATE: 2000-10-20 PRIOR FILING DATE: 2000-10-30 PRIOR FILING DATE: 2000-09-08 NUMBER OF SEQ ID NOS: 207012 SEQ ID NO 8151 LENGTH: 249 TYPE: PRT TYPE	Nearch
1488 88 6. 1490 88 6. 1491 88 6. 1492 88 6. 1493 87.5 6. 1496 87.5 6. 1498 87.5 6. 1499 87.5 6.	RESULT 1 US-09-949-016-8151 Sequence 8151, App Patent No. 6812339 Fatent No. 6812339 TITLE OF INVENTIC TITLE OF INVENTIC TITLE OF INVENTIC TITLE OF INVENTIC CURRENT FILING DATE FILE REFERENCE: C CURRENT FILING DATE PRIOR APPLICATION PRIOR FILING DATE PRIOR FILING	Query Match Beet Local Similarity Matches 247; Conser QY 1 MGLSIFLLL Db 3 MGLSIFLLL QY 61 AHCSGSRYW QY 121 TSSVQFLPL Db 122 TSSVQFLPL Db 122 TSSVQFLPL QY 181 TSNMVCAGG QY 241 IRMIMRNN QY 241 IRMIMRNN QY 242 IRMIMRNN NS-09-949-016-6948 18-09-949-049 NS-09-949-06-6948 18-09-949-049 Patent NO. 6812339 18-00-9413 Applic Patent NO. 6812339 18-00-941 Applic
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121 ISSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRI 180
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GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: O'Brien, Lowell J.
TITLE OF INVENTION: No. 6642013el Extracellular Serine Protease TITLE OF INVENTION: No. 6642013el Extracellular Serine Protease CURRENT APPLICATION NUMBER: US/09/618,259
CURRENT FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: US 09/127,444
PRIOR APPLICATION NUMBER: US 09/127,444
PRIOR APPLICATION NUMBER: 1998-08-21
NUMBER OF SEQ ID NOS: 72
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APPLICANT: SOUTHAN, CHRISTOPHER
APPLICANT: BUNGESS, NICOLA
APPLICANT: BUNGESS, NICOLA
CORRESPONDENCES: 4
CORRESPONDENCES: 4
CORRESPONDENCE ADDRESS:
STREET: P.O. BOX 980
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45.9%; Score 630.5; L
Best Local Similarity 50.2%; Pred. No. 2.5e-
Matches 123; Conservative 24; Mismatches
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; Patent No. 6642013
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ORGANISM: Homo sapiens
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    APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR PELLING DATE: 2000-10-3

PRIOR FILING DATE: 2000-10-03

PRIOR PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TSNMVCAGGVPGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYIC 235
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TITLE OF INVENTION: Human Serine Protease and Serpin Polypeptides
TITLE REPERENCE: PP191

CURRENT APPLICATION WOMBER: US/09/244,111

CURRENT FILING DATE: 1999-02-04

EARLIER APPLICATION NUMBER: 60/073,961

BARLIER APPLICATION NUMBER: 60/073,961

SARLIER OF SEQ ID NOS: 13

SOFTWARE: PATENTIN Ver. 2.0
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Pred. No. 3.8e-71;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94.7%; Score 1301; DB 4; I
100.0%; Pred. No. 1.5e-118;
ive 0; Mismatches 0;
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Sequence 6, Application US/09244111
Patent No. 6566498
GENERAL INFORMATION:
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Best Local Similarity 64.1%;
Matches 159; Conservative (
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Best Local Similarity 100.
Matches 235; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Human
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62 HCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGAS-TSHEHDLRLLRLRLPVRV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  133 GDKVKPVQLANLCPKVGQKCIISGWGTVTSPQENPPNTLNCAEVKIYSQNKCERAYPGKI 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 IFLLLCV----LGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .5e-52
                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: 1BM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastsEO for Windows Version 2.0
SOFTWARE: VAPLICATION DAYS
APPLICATION NUMBER: US/09/025,059
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/09008271A Patent No. 6203979 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Bandman, Olga
Hillman, Jennifer
                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT: INFORMATION:
NAME: BILLINGS, LUGY J
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: PF-04
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yue, Henry
Guegler, Karl J.
Corley, Neil C.
Tang, Tom Y.
Shah, Purvi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49.08;
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LENGTH: 260 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                         650-855-0555
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Matches 121; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 650-845-4166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
  Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INBRARY: General 1020091
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                                      USA
                                                        94304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TSNMVCAGGVPGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDW 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TDGMVCAGSSKGADTCQGDSGGPLVCDGALQGITSWGS-DPCGRSDKPGVYNICRYLDW 251
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Patent No. 6075136
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Corley, Neil C.
APPLICANT: Karl J.
TITLE OF INVENTION: PROSTATE-ASSOCIATED SERINE PROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92; Indels
                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,526
FILING DATE: 30-APR-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . No. 6.2e-53
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                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9711952.3
FILING DATE: 9-JUN-1997
APPLICATION NUMBER: EP 97309646.4
FILING DATE: 1-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-30353
TELEPHONE: 610-407-0700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: PROSTAC
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmac
STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              260 amino acids
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Matches 122; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 260 amino acid
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VALLEY FORGE
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252 IK 253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 TSNWYCAGGVPGQDACQGDSGGPLYCGGYLQGLYSWGSYGPCGQDGIPGYYTYICKYVDW 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 TSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRI
                                                                                                                                                                                                                                                                                                                                                                                                                                               5 IFLLLCV---LGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAA
                                                                                                                                                                                            FEATURE:
OTHER INFORMATION: Amino acid sequence of mouse neuropsin homologous
OTHER INFORMATION: to TADG-14; accession no. D30785
US-09-618-259-8
                                                                                                                                                                                                                                                                                                                                    Length 260
                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                              Query Match
45.3%; Score 622.5; DB 4;
Best Local Similarity 49.0%; Pred. No. 1.5e-52;
Matches 121; Conservative 28; Mismatches 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: PZ007P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EARLIER APPLICATION NUMBER: PCT/US98/11422
EARLIER FILING DATE: 1998-06-04
EARLIER FILING DATE: 1998-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER PEDICATION NUMBER: 60/049,375
EARLIER PEDICATION NUMBER: 60/048,881
EARLIER FILING DATE: 1997-06-06
EARLIER PILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/205,258
PRIOR APPLICATION NUMBER: US 09/127,444
PRIOR FILING DATE: 1998-08-21
NUMBER OF SEQ ID NOS: 72
LENGTH: 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EARLIER APPLICATION NUMBER: 60/048,895
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EARLIER APPLICATION NUMBER: 60/048,971
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,964
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APPLICATION NUMBER: 60/048,971
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 427, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT FILING DATE: 1998-12-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EARLIER APPLICATION NUMBER: 60/
EARLIER FILING DATE: 1997-06-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IKKTWDN 258
                                                                                                                                       TYPE: PRT
ORGANISM: Mus sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 TSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   133 GSKVKPISLADHCTQPGQKCTVSGWGTVTSPRENFPDTLNCAEVKIFPQKKCEDAYPGQI 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           193 TDGMVCAGSSKGADTCQGDSGGPLVCDGALQGITSWGS-DPCGRSDKPGVYTNICRYLDW 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 MFLLLLGGAWAGHŚRAQEDKVLGGHECQPHSQPWQAALSQGQQLLCGGVLVGGNWVLTAA 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 IFLLL---CVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Underwood, Lowell J.
TILLE OF TO NO. 6642013el Extracellular Serine Protease
FILE REFERENCE: D6020CIP2
CURRENT APPLICATION NUMBER: US/09/618,259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94; Indels
                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version 2.0
                            ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Dr. CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 45.3%; Score 622.5; DB 3 Best Local Similarity 49.8%; Pred. No. 1.5e-52; Matches 122; Conservative 24; Mismatches 94
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: «Unknown»
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: MOHAN-PELETSON, Sheela
REGISTRATION NUMBER: 41,201
REFERENCE/DOCKET NUMBER: PF-0458 US
                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/008,271A
FILING DATE: 16-Jan-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLONE: 1798496
SEQUENCE DESCRIPTION: SEQ ID NO: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 260 amino acids
TYPE: amino acid
STRANDEDNESS: single
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Patent No. 6642013
                                                                                                                                                                                                                              MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ropology: linear
                                                                                                                                            USA
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                                                                                                                STATE: CA
COUNTRY: U
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IKKII 256
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123 TWAVRPLTLSSRCVTAGTSCLISGWGSTSSPOLRLPHTLRCANITIIEHOKCENAYPGNI 182
                                                                                                                                                                                    63 CLKPRYIVHLGQHNLQKEEGCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVSI 122
                                                                                                                                                        TSNMVCAG-GVPGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Corley, Neil J.
APPLICANT: Guegler, Karl J.
TILLE OF INVENTION: PROSTATE-ASSOCIATED SERINE PROTEASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indela
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Mismatches 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Dr. CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF-0481 US
                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 1, Application US/09025059; Patent No. 6075136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
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TELEFAX: 650-845-4166
TELEX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 48.29
Matches 120, Conservative
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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242 WIQETMKNN 250
                                                                                                                                                                                                                                                     240 WIRMIMRNN 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: si
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US-09-025-059-1
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48.2%; Pred. No. 3.5e-52;
Live 35; Mismatches 89; Indels 5
EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,892

EARLIER FILING DATE: 1997-06-06

EARLIER FILING DATE: 1997-
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ORGANISM: Homo sapiens
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Best Local Simi
Matches 120;
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CSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGA--STSHEHDLRLLRLRLPVRV 120

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CSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGA--STSHEHDLRLLRLRLPVRV 120

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                                                                                                                    181 TSNMVCAG-GVPGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVD 239
                                                                                                                                      51 KIVGGYNCLEPHSQPWQAALFQGQQLLCGGVLVGGNWVLTAAHCKKPKYTVRLGDHSLQN 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80 LDWTEQIRHSGFSVTHPGYLGAST-SHEHDLRLLRLRLPVRVTSSVQPLPLPNDCATAGT 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        139 ECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRITSNMVCAGGVPGQDACQG 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            171 KCTVSGWGTVTSPRENFPDTLNCAEVKIFPQKKČEDAYPGQITDGMVCAGSSKGADTCQG 230
CLKPRYIVHLGQHNLQKEEGCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVSI 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 KIFNGTEC-GRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAHCSGSRYWVRLGEHSLSQ 79
                                                                OTHER INFORMATION: Description of Artificial Sequence: Fusion gene OTHER INFORMATION: with homo sapien serine protease catalytic domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDWIRMIM 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43.9%; Score 602.5; DB 4; 51.1%; Pred. No. 1.5e-50; tive 21; Mismatches 87;
                                                                                                                                                                                                                                                                                                                          Sequence 13, Application US/09386642
Fatent No. 6420157
GENERAL INFORMATION:
APPLICANT: Darrow, Andrew
APPLICANT: Oi, Jenson
APPLICANT: Andrede-Gordon, Patricia
TITLE OF INVENTION: Zymogen Activation System
FILE REFERENCE: ORT-1028
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 13
LENGTH: 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 14, Application US/09386642
Patent No. 6420157;
General Information:
General Information:
APPLICANT: Darrow, Andrew
APPLICANT: Darrow, Andrew
APPLICANT: Qi. Jenson
TITLE OF INVENTION: Zymogen Activation System
FILE REFERENCE: ORT-1028
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 116, Conservative
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                                                                                                                                                                                              240 WIRMIMRNN 248
                                                                                                                                                                                                                              274 WIQETMKNN 282
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Best Local Similarity
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AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES OF THE PROSTATE
                                                                                                                                                                                                                                                                                                            80 LDWTEQIRHSGFSVTHPGYLGA--STSHEHDLRLLRLRLPVRVTSSVQPLPLPNDCATAG 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRITSNMVCAG-GVPGQDAC 196
                                                                                                                                                                                                                                                                                   21 KIFNGTEC-GRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAHCSGSRYWVRLGEHSLSQ
                                                                                                                                                                                                                                           Gaps
                                                                                                          OTHER INFORMATION: Description of Artificial Sequence: Fusion gene OTHER INFORMATION: with homo sapien serine protease catalytic domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   197 QGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDWIRMIMRNN 248
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                                                                                                                                                                                                  DB 4; Length 289;
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                                                                                                                                                                                             Query Match
43.6%; Score 598.5; DB 4;
Best Local Similarity 49.1%; Pred. No. 3.8e-50;
Matches 114; Conservative 34; Mismatches 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATE
PILLING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6183.US.01
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 24, Application US/08944483
; Patent No. 6232456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COLPITTS, TRACEY L. FRIEDMAN, PAULA N. GRANADOS, EDWARD N. KLASS, MICHAEL R. RUSSELL, JOHN C. STEWART, KRNT C. STEWURE, STEVEN D. STROUPE, STEVEN D.
SEQ ID NO 14
LENGTH: 289
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92
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MEDIUM TYPE: Diskette
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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US-08-956-267A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGA--STSHEHDLRLLRLRLPVRV 120
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STREET: 405 Lexington Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 LOLILLALATGLVGGET-RIIKGFEC-PHSQPWQAALFK-TRLLCGATLIAPRWLLTAAH 60
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Patent No. 5945328
GENERAL INFORMATION:
APPLICANT: WOLDIKE, Helle Fabricius
APPLICANT: KJELDSEN, Thomas Borglum
TITLE OF INVENTION: A Process For Producing Trypsin
TITLE OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE:
COUNTRY: USA

ZIP: 10174
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPALIDLE
COMPUTER: STATE
CLASSIFICATION:
NAME: CAICA
NAME: ROZEK, CAICA
REGISTRATION NUMBER: 36,993
REFERENCE/DOCKET NUMBER: 4500.204-US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION IN
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;; Pred. No. 3.9e-50;
36; Mismatches 87
                                                                                                                                                                                   ; MOLECULE TYPE: No. 6232456e
US-08-944-483-24
                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 47.8%;
Matches 119; Conservative 3
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INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 247 amino acids TYPE: amino acid TOPOLOGY: linear
         INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 248 amino acids
                                                                                            TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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US-08-956-267A-2
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Sequence 8166, Application US/09949016

Patent No. 681239

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
ITILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: CLOOL1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTMARE: PEASESQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 TSSVQPLPLP-NDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGR 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          150 İGYIĞILPLSHNNRLİPGITCRVSGWGTTISPQVNYPKTLQCANIQLRSDEECRQVYPGK 209
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                                                                                                                                                                                                                                                                                                                     SSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRIT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182 GNMICVGFLEGGKDSCQCDSGGPVVCNGQLQGIVSWGY--GCAQKNKPGVYTKVCNYVNW 239
                                                                                                                                                                                                                                                                                       62 HCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRRLPVRVT 121
                                                                                                                                                                                                                                      63
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                                                                                                                                83; Indels
                                                                            Score 573; DB 2;
Pred. No. 9.3e-48;
                                                                                                                                42; Mismatches
                                                                          Query Match
Best Local Similarity 45.6%;
Matches 113; Conservative 42
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Best Local Similarity 46.8 Matches 116; Conservative
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 IRMIMRNN 248
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239 DWIRMIMR 246 ||| :| 269 LWIRETIR 276

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Search completed: March 5, 2005, 17:58:17 Job time : 52 8ecs

Sequence Sequence

Scoring table:

Sequence:

protein

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Minimum DB s Maximum DB s

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Sequence 72, Appl
Sequence 32, Appl
Sequence 395, Appl
Sequence 395, Appl
Sequence 395, Appl
Sequence 52, Appl
Sequence 7, Appli
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Sequence 609, Appli
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Sequence 28, Appl
Sequence 13, Appl
Sequence 657, Appl
Sequence 90, Appl
Sequence 3, Appli
Sequence 3, Appli
Sequence 611, Appli
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Sequence 14, App
Sequence 68, At
Sequence 67, App
Sequence 67, App
Sequence 27, App
Sequence 29, App
Sequence 54, App
Sequence 54, App
Sequence 26, App
Sequence 212, App
Sequence 212, App
Sequence 212, App
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1 US-10-223-082-72
1 US-10-461-781-7
1 US-10-461-781-7
2 US-10-162-521A-395
2 US-10-10-283-395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ITSNMVCAGGVP-GODACOGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYV 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 AAHCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPVR 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 IFLLLCVLGLS-----QAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
41.4%; Score 569.5; DB 2; Length 2
Best Local Similarity 47.5%; Pred. No. 6e-39;
Matches 116; Conservative 39; Mismatches 78; Indels
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A, Residues: 9-231 <HBR>
A, Residues: 9-231 <HBR>
A, Residues: 9-231 <HBR>
A, Note: at position 20. Ile and Val occur alternatively
C, Superfamily: trypsin; trypsin homology
C, Keywords: hydrolase; pancreas; polymorphism; protein digestion; serine proteinase;
F, 1-231/Product: trypsin peptide #status experimental <APT>
F, 9-231/Product: trypsin #status experimental <AMT>
F, 9-231/Product: trypsin #status experimental <AMT>
F, 9-234/Domain: trypsin homology <TRY>
F, 9-24/Domain: trypsin homology <TRY>
F, 9-24/Domain: trypsin homology <TRY>
F, 117-218, 124-191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-1191, 156-
A;Accession: S71155
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-102,'A',104-248 < WANS>
A;Cross-references: EMBL:U15156; NID:g603904; PIDN:AAA79913.1; PID:g603905
A;Experimental source: clone 1-P38
A;Experimental source: clone 1-P38
C;Superfamily: trypsin; homology
C;Superfamily: trypsin; rrypsin homology
C;Reywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen
F;1-15/Domain: signal sequence #status predicted <SIG>F;1-5/Domain: activation peptide #status predicted <APT>
F;26-248/Product: trypsin I #status predicted <MAT>
F;6-241/Domain: trypsin homology <TRX>
F;6-241/Domain: trypsin homology <TRX>
F;6-109,202/Active site: His, Asp, Ser #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118 AATLNSYVNTVPLPTSCVTAGTTCLISGWGNTLSSGSLYPDVLQCLNAPVLSSSQCSSAY 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57 VLTAAHCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             177 PGRITSNMVCAGGV-PGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYIC 235
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N;Contains: trypsinogen
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 24-Apr-1984 #sequence revision 24-Apr-1984 #text_change 09-Jul-2004
C;Accession: A90641; A90368; A00947
R;Charles, M; Rovery, M; Guidoni, A.; Dešnuelle, P.
Biochim: Biophys. Acta 69, 115-129, 1963
A;Title: Su le trypsinogene et la trypsine de porc.
A;Reference number: A90641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MKFLVLVAFLGVAVAFPISDEDDDKIVGGYSCARSAAPYQVSLNSGYHF-CGGSLISSQW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 PVRVTSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 LSIFILLCVLG-----LSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRW
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A; Residues: 1-10 < CHA>
A; Residues: 1-10 < CHA>
A; Residues: 1-10 < CHA>
A; Residues: 1-10 < CHA>
A; Residues: 1-10 < CHA>
A; Residues: 1-10 < CHA>
A; Residues: 1-10 < CHA>
A; Residues: 1-10 < CHA>
A; Residues: 1-10 < CHA>
A; Reference number: 490368; MuID: 73258692; PMID: 4738933
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46.7%; Pred. No. 2.7e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 41.3%; Score 567; DB 2; Best Local Similarity 45.5%; Pred. No. 9.6e-39; Matches 115; Conservative 38; Mismatches 88
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C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
C;Accession: A53968
B;Hansson, L; Stroemqvist, M.; Baeckman, A.; Wallbrandt, P.; Carlstein, A.; Egelrud, T.
J. Biol. Chem. 269, 19420-19426, 1994
A;Title: Cloning, expression, and characterization of stratum corneum chymotryptic enzyme A;Accession: A53968
A;Accession: A53968
A;Status: preliminary
A;Molecule Cype: mRNA
A;Residues: 1-253 cHAN>
A;Residues: 1-253 cHAN>
A;Cross_references: UNIPROT:P49862; GB:L33404; NID:g521214; PIDN:AAC37551.1; PID:g532504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 trypsin (EC 3.4.21.4) precursor - mouse (5Species: Mus musculus (house mouse) (c)Species: Mus musculus (house mouse) (c)Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004 (c)Accession: B25528 (c)Accession: B25528 (c)Accession: B.J.; Hagenbuechle, O.; Wellauer, P.K. (c)Accession: B.J.; Hagenbuechle, O.; Wellauer, P.K. (c)Acids Res. 14, 8307-8330, 1986 (c)Aritle: Sequence organisation and transcriptional regulation of the mouse elastase II (c)Accession: B25528 (c)Accession: B25528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-246 <STES.
A; Residues: 1-246 <STES.
A; Cross-references: UNIPROT: P07146; GB:X04574; NID:954918; PIDN:CAA28243.1; PID:954919
C; Superfamily: trypsin; trypsin homology
C; Superfamily: trypsin; trypsin proclamse; protein digestion; serine proteinase
F; 1-23/Domain: signal sequence #status predicted <SIG>F; 24-246/Product: trypsin homology <TRY>
F; 24-236/Product: trypsin homology <TRY>
F; 24-239/Domain: trypsin homology <TRY>
F; 30-100, A8-64, 132-233, 139-206, 171-188/Disulfide bonds: #status predicted
F; 30-100, A8-64, 134, A8p, Ser #status predicted
F; 35, 77, 80, 85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         113 RLRLPVRVTSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATC 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MGLSIFLLLCVLGLS-----QAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          177 TKVYKDLLENSMLCA-GIPDSKKNACNGDSGGPLVCRGTLQGLVSWGTF-PCGQPNDPGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 LSIFLLLCVLGLSQA----ATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40.4%; Score 555; DB 2; 44.6%; Pred. No. 9.2e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37; Mismatches
                                                                                                                                                                                                                                                                                                                                   A,Cross-references: GDB:377730
A,Map postition: 7q35-7q35
C;Superfamily: trypsin; trypsin homology
F;30-245/Domain: trypsin homology <TRY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              235 YTQVCKFTKWINDTMKKH 252
                                                                                                                                                                                                                                                                                   C,Genetics:
A,Gene: GDB:PRSS6; SCCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 44.6
Matches 115; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 44., les 113; Conservative
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A. Status: preliminary
A. Molecule type: mRNA
A. Molecule type: mRNA
A. Residues: 1-243 < SHI>
A. Cross-references: UNIPROT:P19799; EMBL:XS3458; NID:g65162; PIDN:CAA37538.1; PID:g65163
C. Superfemily: trypsin; trypsin; trypsin; trypsin; trypsin; trypsin; trypsin; serine proteinase
F. 1-15/Domain: signal sequence #status predicted < SIG>
F. 16-20/Domain: activation peptide #status predicted < APT>
F. 21-236/Domain: trypsin I #status predicted < NAT>
F. 24-35/Domain: trypsin I #status predicted < NAT>
F. 26-243/Product: trypsin I #status predicted < NAT>
F. 26-243/Product: trypsin I #status predicted < NAT>
F. 27-157, 45-61, 129-230, 136-203, 168-182/Disulfide bonds: #status predicted
F. 60, 104, 197/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Xenopus laevis (African clawed frog)
C;Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 09-Jul-2004
C;Accession: A35871; S12117
R;Shi, Y.B.; Brown, D.D.
A;Shi, Y.B.; Brown, D.D.
A;Title: Developmental and thyroid hormone-dependent regulation of pancreatic genes
A;Reference number: A35871; MUID:91007255; PMID:2210372
                                                                                                                                                                                     CYKASIQVRLGEHNIALSEGTEQFISSSKVIRHSGY--NSYTLDNDIMLIKLSSPASLNA 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPVRVTS 122
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                                                                                                      KIVGGYTCAANSIPYQVSLNSGSHF-CGGSLINSQWVVSAAHCYKSRIQVRLGEHNIDVL
                                                                                                                                                        DWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPVRVTSSVQPLPLPNDCATAGTEC
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          Gaps
                                                                                                                                                                                                                                                                                                                                                             SGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDWIRMIMRNN 248
                                                                                                                                                                                                                                                                                                                                                                                          pancreatic - African clawed frog
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          77; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40.4%; Score 555; DB 2;
45.7%; Pred. No. 8.8e-38;
cive 42; Mismatches 82;
       Mismatches
       39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          trypsin (EC 3.4.21.4) precursor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 45.7<sup>3</sup>
Matches 113, Conservative
       107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RMIMRNN 248
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C.jpecies: Bos primigenius (cattle)
C;paccies: Bos primigenius taurus (cattle)
C;pate: 02-Dec-1993 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C;Date: 02-Dec-1993 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C;Accession: S13813
R;Le Huerou, I: Wicker, C.; Guilloteau, P.; Toullec, R.; Puigserver, A.
Bur, J. Biochem. 193, 767-773, 1990
A;Title: Isolation and nuclectide sequence of cDNA clone for bovine pancreatic anionic than the ference number: S13813; MUID:91065383; PMID:1701147
A;Reference number: S13813
A;Stetus: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                trypsin (EC 3.4.21.4) precursor, anionic - dog
NiAlternate names: cationic trypsinogen
NiAlternate names: cationic trypsinogen
NiAlternate names: cationic trypsinogen
C;Species Canis lupus familiaris (dog)
C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
C;Accession: A26273
R;Pinsky, S.D.; LaForge, K.S.; Scheele, G.
Mol. Cell. Biol. 5, 2669-2676, 1985
A;Title: Differential regulation of trypsinogen mRNA translation: full-length mRNA seque
A;Reference number: A26273; MUID:86284628; PMID:3841794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: mRNA
A;Residues: 1-247 <PIN>
A;Cross-references: UNIPPOT:P06872; GB:M11589; NID:g164094; PIDN:AAA30899.1; PID:g164095
C;Superfamily: trypsin; trypsin; homology
C;Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen
F;1-15/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Modecule type: mRNA
A; Residues: 1-247 <-HUE>
A; Cross-references: UNIPROT: Q29463; EMBL: X54703; NID: 9829; PIDN: CAA38513.1; PID: 9830
C; Superfamily: tryppsin homology
C; Keywords: hydrolase; protein digestion; serine proteinase
F; 24-239/Domain: trypsin homology <-TRY>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 CYQYHIQVRLGEYNIDVLEGGEQFIDASKIIRHPKY--SSWTLDNDILLIKLSTPAVINA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123 SVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRITS 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       141 HVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRITSNMVCAGGVP-GQDACQGD 199
                       123 LISGWGNTKSSGTSYPDVLKCLKAPILSDSSCKSAYPGQITSNMFCAGYLEGGKDSCQGD 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 LLLCVIGLSQA----ATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAH
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                                                                                                       183 SGGPVVCSGKLQGIVSWGS--GCAQKNKFGVTKVCNYVSWIKQTIASN 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
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40.0%; Score 550; DB 2;
Best Local Similarity 45.7%; Pred. No. 2.3e-37;
Matches 113; Conservative 40; Mismatches 84.
                                                                                                                                                                                                                                trypsin (EC 3.4.21.4) - bovine
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                                                                                          176
                                                                                                                                                                          PGRITSNMVCAGGVP-GQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYIC 235
                                                                                                                                                                                                  KIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAHCSGSRYWVRLGEHSLSQL 80
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                                                                                                                                                                                                                                                                                                                                                                                                trypsin (EC 3.4.21.4) precursor - bovine
NyContains: trypsinogen
C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Accession: A90164; A00946; Say 174
R;Mikes, O.; Holeysovsky, V.; Tomasek, V.; Sorm, F.
Biochem: Biophys. Res. Commun. 24, 346-352, 1966
A;Title: Covalent structure of bovine trypsinogen. The position of the remain A;Reference number: A90164; MUID:67168848; PMID:5967094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 TAAHCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLFLPV
                                                                                                                  RVTSSVQPLPLPNDCATAGTECHVSGWG--ITNHPRNPFPDLLQCLNLSIVSHATCHGVY
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40.2%; Score 552; DB 1; Length 22
Best Local Similarity 46.3%; Pred. No. 1.4e-37;
Matches 106; Conservative 40; Mismatches 77; Indels
                                                                                                                                                                                                                                                               236 KYVDWIRMIMRNN 248
                                                                                                                                                                                                                                                                                         |||||: ::|
234 NYVDWIQNTIADN 246
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A;Accession: A27547
A;Molecule type: mRNA
A;Rossiduse: 1-247 <FLES
C;Superfamily: trypsin homology
C;Superfamily: trypsin homology orRxy.
F;32-240/Domain: trypsin homology orRxy.
F;32-240/Domain: trypsin homology orRxy.
F;31-161, 49-65, 113-234, 140-207, 172-186/Disulfide bonds: #status predicted
F;64,108,201/Active site: His, Asp, Ser #status predicted
F;76, 78,81,86/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                            C;Species: Rattus norvegicus (Norway rat)
C;Dacate: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
C;Daccession: A27547
R;Fletcher, T.S.; Alhadeff, M.; Craik, C.S.; Largman, C.
Biochemistry 26, 3081-3086, 11987
Biochemistry 26, 3081-3086, 11987
A;Title: Isolation and characterization of a cDNA encoding rat cationic trypsinogen. A;Title: A27547; MUID:8721609; PMID:3607011
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N;Alternate names: trypsinogen I
C;Species: Rattus norvegicus (Norway rat)
C;Date: 17-Dec-1982 #sequence_revision 17-Dec-1982 #text_change 09-Jul-2004
C;Accession: B22657; A00948
E;Craik, C.S.; Choo, Q.L.; Swift, G.H.; Quinto, C.; MacDonald, R.J.; Rutter, W.J.
J. Biol. Chem. 259, 14255-14264, 1984
A;Title: Structure of two related rat pancreatic trypsin genes.
A;Reference number: A22657; MUID:85054880; PMID:6094547
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 VSAAHCYKSRIQVRLGEHNIDVVEGGEQFIDAAKIIRHPSY--NANTFDNDIMLIKLNSP 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118 VRVISSVQPLPLPNDCATAGTECHVSGWGIINHPRNPPPDLLQCLNLSIVSHATCHGVYP 177
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         237
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      179 RITSNMVCAGGVP-GQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKY
                                      3 LSIFLLLCVLGLSQAA----TPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWV
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                                                                                                                                                                                                                                                                                                                                                  trypsin (EC 3.4.21.4) precursor, cationic - rat
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                                                                                                                                238 VDWIRMIMRNN 248
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A; Residues: 1-246 < CRA>
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Mosidues: 1-246 cPIN>
A; Mosidues: 1-246 cPIN>
A; Cross-references: UNIPROT: P06871; GB: M11590; NID: g164096; PIDN: AAA30900.1; PID: g164097
C; Superfamily: trypsin; trypsin homology
C; Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen
C; Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen
C; Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen
F; 16-23/Domain: activation peptide #status predicted <ARI>
F; 24-246/Product: trypsin, cationic #status predicted <ARI>
F; 24-239/Domain: trypsin, homology <ARI>
F; 24-239/Domain: trypsin, homology <ARI>
F; 24-230/Domain: trypsin, homology <ARI>
F; 24-230/Active aite: His, Asp, Ser #status predicted
F; 63, 107, 200/Active aite: Galcium (Glu, Asn, Val, Glu) #status predicted
F; 75, 77, 80, 85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted
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NyAlternate names: cationic trypsinogen
C;species: canis lupus familiaris (dog)
C;bacesion: B26273
R;pinsky, S.D.; LaForge, K.S.; Scheele, G.
Mol. Cell. Biol. 5, 2669-2676, 1987
A;ritle: Differential regulation of trypsinogen mRNA translation: full-length mRNA s A;Reference number: A26273; MUID:86284628; PMID:3841794
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 ENMICAGFLEGGKDSCQGDSGGPVVCNGELQGIVSWGY--GCAQKNKPGVYTKVCNFVDW 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 TAAHCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPV 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNMVCAGGVP-GQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDW 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RVTSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118 TLNSRVSAIALPKSCPAAGTQCLISGWGNTQSIGQNYPDVLQCLKAPILSDSVCRNAYPG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPVRVT 121
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                                                                                                                                                                                                                                                                                                                                                                                         3 LSIFLLLCVLGLSQA----ATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVL
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P;24-247/Product: trypsin, anionic #status predicted <ENZ>
P;24-239/Domain: trypsin homology <TRY>
P;30-160,48-64,132-233,139-206,171-185/Disulfide bonds: #status predicted P;30-107,200/Active site: His, Asp, Ser #status predicted F;75,77,80,85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted
                                                                                                                                                                                                                                                                                                                                                  7 LLLCVLGLSQAATP----KIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAA
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                                                                                                                                                                                                                                                                                     12;
                                                                                                                                                                                                                    39.7%; Score 546; DB 1; Length 247; larity 45.6%; Pred. No. 4.8e-37; Conservative 38; Mismatches 85; Indels 1
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44.2%; Pred. No. 5.8e-37;
tive 43; Mismatches 87;
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Matches 111, Conservative
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Best Local Simi
Matches 113;
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A;Molecule type: mRNA
A;Residues: 1-247 <LUE>
A;Cross-references: UNIPROT:P12788; EMBL:X15679; NID:g56813; PIDN:CAA33718.1; PID:g56814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Cross-references: UNIPROT:P12788; EMBL:X15679; N1D:950813; riun:Langerianity: trypsin; trypsin; homology
C; Superfamily: trypsin; trypsin; hydrolase; protein digestion; serine proteinase; zymogen
C; Keywords: calcium binding; hydrolase; protein digestion; serine proteinase; zymogen
F;1-15/Domain: signal sequence #status predicted <ABT>
F;24-24/Product: trypsin IV #status predicted <AMT>
F;24-24/Product: trypsin IV #status predicted <AMT>
F;24-24/Domain: trypsin homology <TRY>
F;30-161,49-65,133-234,140-207,172-186/Disulfide bonds: #status predicted
F;64,108,201/Active site: His, Asp, Ser #status predicted
F;76,78,81,86/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted
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                                        81 DWTEQIRHSGPSVTHPGYLGASTSHEHDLRLLRLRLPVRVTSSVQPLPLPNDCATAGTEC 140
                                                                        HVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRITSNMVCAGGVP-GQDACQGD 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        trypsin (EC 3.4.21.4) IV precursor - rat
N,Alternate names: 23K protein; trypsinogen IV precursor
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
                                                                                                                                                                                               1 MGLSIF -- LLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               179 RITSNMVCAGGVP-GQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: S05494

R;Luetcke, H.; Rausch, U.; Vasiloudes, P.; Scheele, G.A.; Kern, H.F.
Nucleic Acids Res. 17, 6736, 1989

A;Title: A fourth trypsingen (P23) in the rat pancreas induced by CCK.
A;Reference number: S05494; MUID:89386010; PMID:2780302
A;Accession: S05494
                                                                                                                                                                                                                                                                                                                       SGGPVVCNGQLQGVVSWGY--GCAQRNXPGVYTKVCNYRSWISSTMSSN 238
                                                                                                                                                                                                                                                                                    200 SGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDWIRMIMRNN 248
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Best Local Similarity 43.4%; Pred. No. 4.9e-36;
Matches 109; Conservative 41; Mismatches 94
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Job time : 53 secs
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                                            8
A;Title: Two similar but nonallelic rat pancreatic trypsinogens. Nucleotide sequences of A;Reference number: A00948; MUID:82265624; PMID:6896710
A;Accession: A00948
A;Molecule type: RRNA
A;Mosidues: 1-246 cMAC>
A;Cross-references: GB:J00778; NID:g206507; PIDN:AA98518.1; PID:g206508
C;Genetics:
A;Introns: 14/1; 67/2; 152/1; 197/3
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; pancreas; protein digestion; serine proteinase; zymogen
F;1-15/Domain: activation peptide #status predicted cSIG>
F;1-23/Domain: activation peptide #status predicted cAPT>
F;24-234/Product: trypsin I #status predicted cENZ>
F;24-234/Product: trypsin I #status predicted cENZ>
F;34-239/Domain: activation peptide #status predicted cENZ>
F;30-160,48-64,132-233,139-206,171-185/Disulfide bonds: #status predicted
F;63,107,200/Active site: His, Asp, Ser #status predicted
F;75,77,80,85/Binding site: calcium (Glu, Asn, Val, Glu) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              trypsin (EC 3.4.21.4) III precursor - Atlantic salmon (fragment)
C;Species: Salmo salar (Atlantic salmon)
C;Species: 22-Nov-1993 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C;Accession: 866657; 831779; 831798
R; Lorens, J.B.; Smalas, A.O.; Torrissen, K.R.
Bur. J. Biochem. 232, 677-685, 1995
A;Title: Molecular cloning and characterization of anionic and cationic variants of tryp. A;Reference number: 866657; MUID:96035908; PMID:7556223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA

A; Residues: 1-238 «MAL»

A; Cross-references: UNIPROT: P35033; EMBL: X70074; NID: 964387; PIDN: CAA49679.1; PID: 964388

C; Superfamily: trypsin; trypsin homology

C; Keywords: hydrolase; serine proteinase

F; 1-7/Domain: signal sequence (fragment) #status predicted «SIG»

F; 1-5/Domain: activation peptide #status predicted «APT»

F; 16-23| Domain: trypsin III #status predicted «MAT»

F; 16-23| Domain: trypsin homology «TRY»

F; 22-152, 40-56, 124-225, 131-198, 163-177, 188-212/Disulfide bonds: #status predicted

F; 55, 99, 192/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59 TAAHCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPV 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SAAHCYKSRIQVRLGEHNINVLEGDEQFINAAKIIKHPNY--SSWTLNNDIMLIKLSSPV 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RVTSSVOPLPLPNDCATAGTECHVSGWG--ITNHPRNPFPDLLQCLNLSIVSHATCHGVY 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PGRITSNMVCAGGVP-GQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYIC 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         176 PGEITSSMICVGFLEGGKDSCQGDSGGPVVCNGQLQGIVSWGY--GCALPDNPGVYTKVC 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 KIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAHCSGSRYWVRLGEHSLSQL 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KIVGGYEČRKNSASYQASLQSGYHF-CGGSLISSTWVVSAAHCYKSRIQVRLGEHNIAVN 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 LSIFLLLCVLGLSQA----ATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39.5%; Score 543; DB 1; Length 246; 44.5%; Pred. No. 8.4e-37; ive 47; Mismatches 76; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39.3%; Score 540; DB 2;
47.2%; Pred. No. 1.4e-36;
tive 37; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 47.2'
Matches 108; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           110; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             234 NFVGWIQ 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KYVDWIR 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60
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Matches
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4

7;

94; DB 2;

Length 247; Indels 28

237 236

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Protein of the invention #54
                      WO200078961-A1.
28-DEC-2000.
(GETH ) GENENTECH INC.
                                                                                             Best Local Similarity RESULT 7
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Best Local Similarity
RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity RESULT 11
                                                                                                                                                                                                                                                                                                 ABO44488 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADD38353 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US2003073129-A1.
                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                4: geneseqp2002s:*
5: geneseqp2003s:*
6: geneseqp2003s:*
7: geneseqp2004s:*
8: geneseqp2004s:*
8: geneseqp2004s:*
8: geneseqp2004s:*
8: geneseqp2004s:*
and is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description
GenCore version 5.1.6

tein search, using sw model

March 5, 2005, 17:55:12; Search time 165 Seconds

(without alignments)

581.313 Million cell updates/sec
                                                                                                                                      1 MGLSIFLLLCVLGLSQAATP......GVYTYICKYVDWIRMIMRNN 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-SEP-2000.

(MOUN ) MOUNT SINAI HOSPITAL.

(MOUN ) MOUNT SINAI HOSPITAL.

lery Match

100.0%; Score 1374; DB 3; Length 248;

lery Match

100.0%; Pred. No. 5e-98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 1374; DB 3; Length 248; 100.0%; Pred. No. 5e-98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 1374; DB 3; Length 248; 100.0%; Pred. No. 5e-98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 1374; DB 4; Length 248; 100.0%; Pred. No. 5e-98;
                                                                                                                                                                                                                      2105692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY99393 standard; protein; 248 AA.
Human PRO1303 (UNQ669) amino acid sequence SEQ ID NO:194.
W0200012708-A2.
09-MAR-2000.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 1374; DB 3; Best Local Similarity 100.0%; Pred. No. 5e-98; RESULT 4
                                                                                                                                                                       Gapop 10.0 , Gapext 0.5
Searched: 2105692 seqs, 386760381 residues
Total number of hits satisfying chosen parameters:
Minimum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB24428 standard; protein; 248 AA.
Human PRO1303 protein sequence SEQ ID NO:203.
WO200032221-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB24032 standard; protein; 248 AA.
Human PRO1303 protein sequence SEQ ID NO:33.
WO200053750-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAM23994 standard; protein; 248 AA.
Human EST encoded protein SEQ ID NO: 1519.
WO200154477-A2.
                                                                                                                                                                                                                                                                                                                    summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB21304 standard; protein; 248 AA.
Human KLK-L5 protein #4.
WO200053776-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB66142 standard; protein; 248 AA
                                                                                                                                                                                                                                                                       Post_processing: Minimum Match 0% Maximum Match 150% Listing first 150% A Geneseq 16Dec04: 1: geneseqp19808:*
                                                                                                                                                                                                                                                                                                                                                                           geneseqp1990s:*
geneseqp2000s:*
geneseqp2001s:*
                                                                                             US-10-006-856A-194
1374
                      OM protein - protein search,
Run on: March 5, 200
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 3
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                                                                                                                                                             BLOSUM62
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(HYSE-) HYSEQ INC.
                                                                                                                                      Sequence:
Scoring table:
                                                                                                  Title:
Perfect score:
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Best Local Si
RESULT 5
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Best Local Si
RESULT 2
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ID AAB21
DE Humar
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PD 14-SE
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17-APR-2003.
(GETH) GENENTECH INC.
(ery Match 100.0%; Score 1374; DB 7; Length 248;
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PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1374; DB 7; Length 248;
Best Local Similarity 100.0%; Pred. No. 5e-98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PD 20-MAR-2003.

PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1374; DB 7; Length 248;

Best Local Similarity 100.0%; Pred. No. 5e-98;
Length 248;
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                                       necossos standard; protein; 248 AA.
Novel human secreted and transmembrane protein PRO1303.US2003073130-A1.
                                                                                                                                                                                                                                                                                                                                                                                ABO33512 standard; protein; 248 AA.
Novel human secreted and transmembrane protein PRO1303.
                                                                                                                                              Query Match 100.0%; Score 1374; DB 6; Best Local Similarity 100.0%; Pred. No. 5e-98; RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-47-2003.
(GETH ) GENENTECH INC.
(GETH ) GENENTECH INC.
(Ery Match 100.0%; Score 1374; DB 7;
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(GETH) GENENTECH INC.
(ery Match 100.0%; Score 1374; DB 7;
ery Match 100.0%; Pred. No. 5e-98;
100.0%; Score 1374; DB 4; 100.0%; Pred. No. 5e-98;
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Pred. No. 5e-98;
                                                                                                                                                                                                                                                                                                                          Score 1374; DB
Pred. No. 5e-98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADD70709 standard; protein; 248 AA.
Human secreted/transmembrane protein PRO1303.
US2003099625-A1.
                                                                                                                                                                                                                                        Human secreted/transmembrane protein PRO1303. US2003044841-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADD39786 standard; protein; 248 AA.
Human secreted/transmembrane protein PRO1303.
US2003083462-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADD70232 standard; protein; 248 AA.
Human secreted/transmembrane protein PRO1303.
US2003054406-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human secreted/transmembrane protein PRO1303. US2003096955-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human secreted/transmembrane protein PRO1303.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADC18063 standard; protein; 248 AA.
Human PRO polypeptide #54.
US2003064925-Al.
                                                                                                                                                                                                                         protein; 248 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein; 248 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADD39309 standard; protein; 248 AA
                                                                                                                                                                                                                                                           PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%;
Best Local Similarity 100.0%;
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22-MAY-2003.
(GETH ) GENENTECH INC.
MATCh 'TOTILY 100.0%;
                                                                                                                   17-APR-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
RESULT 10.
ID ADC18063 standard; pr
DB Human PRO polypeptide
PD 03-APR-2003.
PA (GETH ) GENENTECH INC
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100.0%; Score 1374; DB 7; Length 248; 100.0%; Pred. No. 5e-98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 248;
                                                                                                                                                                                                                                                                                                                  100.0%; Score 1374; DB 7; Length 248; 100.0%; Pred. No. 5e-98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 1374; DB 7; Length 248; 100.0%; Pred. No. 5e-98;
          CZ-MAY-2003.
(GETH) GENENTECH INC.
ery Match 100.0%; Score 1374; DB 7; Length 248;
                                                                                                                                                                               100.0%; Score 1374; DB 7; Length 248; 100.0%; Pred. No. 5e-98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 1374; DB 7; Length 248; 100.0%; Pred. No. 5e-98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PD 01-MAY-2003.

PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1374; DB 7;
Best Local Similarity 100.0%; Pred. No. 5e-98;
RESULT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADE50007 standard; protein; 248 AA.
Human secreted/transmembrane protein PRO1303.
US2003082626-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    лыуузв' standard; protein; 248 AA.
Human secreted/transmembrane protein PRO1303.
US2003065142-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADE21565 standard; protein; 248 AA.
Human secreted/transmembrane protein PRO1303.
US2003082628-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADF55883 standard; protein; 248 AA.
Human secreted/transmembrane protein PRO1303.
US2003204054-A1.
                                                                                              ADD38812 standard; protein; 248 AA.
Human secreted/transmembrane protein PRO1303.
US2003092061-A1.
                                                                                                                                                                                                                                 ADD40263 standard; protein; 248 AA.
Human secreted/transmembrane protein PRO1303.
US2003082627-A1.
                                                                                                                                                                                                                                                                                                                                                                   ADE50484 standard; protein; 248 AA.
Human secreted/transmembrane protein PRO1303.
US2003069179-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DE20096 standard; protein; 248 AA.
Human secreted/transmembrane protein PRO1303.
US2003092883-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-MAY-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                    01-MAY-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2003.
(GETH ) GENENTECH INC
                                                                                                                                             15-MAY-2003.
(GETH) GENENTECH INC.
Ouery Match
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Best Local Similarity
RESULT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity RESULT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity RESULT 19
                                                                                                                                                                                             Best Local Similarity RESULT 17
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                                             Ouery Match
Best Local Similarity
RESULT 16
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US2003096954-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1374; DB 8; Length 248;
Best Local Similarity 100.0%; Pred. No. 5e-98;
PD 03-APR-2003.

PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1374; DB 7; Length 248;

Best Local Similarity 100.0%; Pred. No. 5e-98;

RESULT 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GETH) GENENTECH INC. (GETH) GENENTECH INC. (GETH) GENENTECH 100.0%; Score 1374; DB 8; Length 248; ery Match cimilarity 100.0%; Pred. No. 5e-98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 1374; DB 8; Length 248; 100.0%; Pred. No. 5e-98;
                                                                                                                                                                                                                             Length 248;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 248;
                                                                                                                                                                                                                                                                                                                                                                                                                         ID ADF24777 standard; protein; 248 AA.

DE Human secreted/transmembrane protein PRO1303.

PN US200318993-A1.

PD 23-OCT-2003.

PA (GETH) GENENTECH INC.

QUERY MATCh

Best Local Similarity 100.0%; Pred. No. 5e-98;

RESULT 28
                                                                                                                                                                                                                           Score 1374; DB 8;
Pred. No. 5e-98;
                                                                                                                                                                                                                                                                                                                                                                                          DB 8;
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(GETH ) GENENTECH INC.
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:ry Match 100.0%; Pred. No. 5e-98;
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PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1374; DB Best Local Similarity 100.0%; Pred. No. 5e-98; RESULT 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1374; DB
Pred. No. 5e-98;
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US2004005626-A1.
08-JAN-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADH03082 standard; protein; 248 AA.
Human secreted/transmembrane protein PRO1303.
202003216562-A1.
20-NOV-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADH04036 standard; protein; 248 AA.
Human secreted/transmembrane protein PRO1303.
US2003220471-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADH03559 standard; protein; 248 AA.
Human secreted/transmembrane protein PRO1303.
US200324478-A1.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADE97044 standard; protein; 248 AA.
Human secreted/transmembrane protein PRO1303.
US2003195334-A1.
                                                                                                                           ADE96567 standard; protein; 248 AA.
Human secreted/transmembrane protein PRO1303.
US2003195347-A1.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                        ADF25878 standard; protein; 248 AA.
Human secreted/transmembrane protein PRO1303.
US2003199675-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human secreted/transmembrane protein PRO1303.
US2003203401-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADH04513 standard; protein; 248 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADF29513 standard; protein; 248 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USZUCZ-
30-OCT-2003.
(GETH ) GENENTECH INC.
MATCh ... Match 100.0%;
                                                                                                                                                                                                                           100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
RESULT 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity RESULT 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Length 184;

Length 162;

Query Match

RESULT 36 ID ADL94 DE Human PN US200 PD 15-AP

RESULT 37
ID ADT94
DE Humar
PN AU200
PD 27-NC

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AAY03220 standard; protein; 260 AA.
Amino acid sequence of human tumour antigen derived gene-14 protein.
WO9909138-AI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vuery Match 45.9%; Score 630.5; DB 3; Length 260; Best Local Similarity 50.2%; Pred. No. 1.1e-40; RESULT 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 45.9%; Score 630.5; DB 3; Length 260; Best Local Similarity 50.2%; Pred. No. 1.1e-40; RESULT 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 45.9%; Score 630.5; DB 2; Length 260; Best Local Similarity 50.2%; Pred. No. 1.1e-40; RESULT 48
   94.7%; Score 1301; DB 8; Length 254; 100.0%; Pred. No. 2.2e-92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB44300 standard; protein; 260 AA. Human PR0322 (UNQ283) protein sequence SEQ ID NO:395. W0200053756-A2. 14-SEP-2000. (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 45.9%; Score 630.5; DB 2;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PD 14-SEP-2000.

PA (MOUN) MOUNT SINAI HOSPITAL.

Query Match

Query Match

45.9%; Score 630.5; DB 3;

Best Local Similarity 50.2%; Pred. No. 1.1e-40;

RESULT 49
                                                                                                                                                                                H4-SEP-2000.
(MOUNT SINAI HOSPITAL.
(MOUNT) MOUNT SINAI HOSPITAL.
74.2%; Score 1019; DB 3;
ery Match Anniarity 100.0%; Pred. No. 8.5e-71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 45.9%; Score 630.5; DB 2; Best Local Similarity 50.2%; Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                            #CO.T.C. | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AUGH | 12-AU
                                                                                                                                                                                                                                                                                                                                                       AAY28642 standard; protein; 162 AA.
Human secreted protein from cDNA clone HKAFV61.
WO9940183-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JP11318461-A.
24-NOV-1999.
(SHIO/) SHIOZAKA S.
(IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY32852 standard; protein; 260 AA.
Human serine protease protein sequence.
JP11225765-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY41744 standard; protein; 260 AA. Human PR0322 protein sequence. W09946281-A2. 16-SEP-1999. (GETH ) GENENTECH INC.
                                                                                           ABB21301 standard, protein; 184 AA.
Human KLK-L5 protein #1.
WO200053776-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB21322 standard; protein; 260 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY51131 standard; protein; 260 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU12369 standard; protein; 260 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human PRO322 polypeptide sequence. WO200140466-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human neuropsin protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-FEB-1999.
(UYAR-) UNIV ARKANSAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-AUG-1999.
(SUNR ) SUNTORY LTD.
                    Best Local Similarity RESULT 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
RESULT 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human neuropsin.
WO200053776-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-JUN-200
   Query Match
                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                 Best Loc
RESULT 44
                              Score 1374; DB 8; Length 248;
Pred. No. 5e-98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 1374; DB 8; Length 248; Best Local Similarity 100.0%; Pred. No. 5e-98;
                                                                                                                                                                                                                                                                                          DB 8; Length 248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; Length 248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8; Length 248;
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(MOUN ) MOUNT SINAI HOSPITAL.
ery Match
ery Match
oritisty 100.0%; Pred. No. 2.2e-92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IS-MAY-2003.
(MILL-) MILLENNIUM PHARM INC.
ery Match 99.5%; Score 1367; DB 6; Length 248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94.7%; Score 1301; DB 3; Length 254; 100.0%; Pred. No. 2.2e-92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 254;
                                                                                                                                                                                                                                                                                                                                                                               ADNI0927 standard; protein; 248 AA.

Human kallikrein 12, marker of endocrine cancer.
W02004029285-A2.
08-APR-2004.
(MOUN ) MOUNT SINAI HOSPITAL.
ery Match
st Local Similarity 100.0%; Pred. No. 5e-98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94.7%; Score 1301; DB 5; 100.0%; Pred. No. 2.2e-92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADNI0926 standard; protein; 254 AA.
Human kallikrein 12, marker of endocrine cancer.
WO2004029285-A2.
                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 1374; DB Best Local Similarity 100.0%; Pred. No. 5e-98; RESULT 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 5e-98;
                                                                                                                   ADH61514 standard; protein; 248 AA.
Human secreted/transmembrane protein PRO1303.
US2004014130 A1.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADD94713 standard; protein; 248 AA.
Human secreted/transmembrane protein PRO1303.
US2004073015-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADP56174 standard; protein; 254 AA.
Human PRO protein sequence SEQ ID NO:2150.
WO2004039956-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA029516 standard; protein; 248 AA.
Human kallikrein-like protein 5 (18817).
WO2003039475-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADT94373 standard; protein; 248 AA.
Human PRO1303 protein.
AU2003259607-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB21303 standard; protein; 254 AA.
Human KuK-L5 protein #3.
WO200053776-A2.
14-SEP-2000.
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Human novel polypeptide #11.
WO200244340-A2.
                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MOUN ) MOUNT SINAI HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-APR-2004.
(GETH ) GENENTECH INC.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                           Query Match
Best Local Similarity
RESULT 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
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Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-JUN-2002
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Length 260;

Query Match

Query Match

RESULT 41
ID ADN10
DE Human
PN WO200
PD 08-AP

RESULT 42

Length 260;

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ABO25246 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003050239-A1.
                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 630.5; DB 6; Length 260; Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Length 260;
 Score 630.5; DB 4; Length 260;
Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                      45.9%; Score 630.5; DB 4; Length 260; 50.2%; Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                DB 5; Length 260;
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                                                                                                                         Score 630.5; DB 4; Length 260; Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 5; Length 260;
                                                             Human angiogenesis-associated protein PRO322, SEQ ID NO:127 WO200053753-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABO17813 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003032156-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB95458 standard; protein; 260 AA.
Human angiogenesis related protein PR0322 SEQ ID NO:
WQ200208284-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45.9%; Score 630.5; DB 5; 50.2%; Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                Score 630.5; DB 5
Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                  ABB84852 standard; protein; 260 AA.
Human PRO322 protein sequence SEQ ID NO:72.
WO200200690-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADI17076 standard; protein; 260 AA.
Human NOVX protein homologue SeqID 612.
WO200268649-A2.
                                                                                                                                                                     ABG23373 standard; protein; 260 AA.
Novel human diagnostic protein #23364
w0200175667-A2.
11-OCT-2001.
(HYSE-) HYSEQ INC.
                                                  protein; 260 AA
                                                                                                                                                                                                                                                                                                                                                                                                                             AAU81959 standard, protein; 260 AA
                                                                                                                                                                                                                                                                                                                                                                              45.9%;
   45.9%;
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Best Local Similarity 50.2%;
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2002.
2002.
Lery Match
Best Local Similarity 5.
RESULT 58
ID ABO17813 standar
PD Novel human
PD 13-7
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GURNEX A L.
HILLAN K J.
MARSTERS S A.
PAN J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GERBER H.
GERRITSEN M E.
                                                                                               14-SEP-2000.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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WATANABE C K.
WILLIAMS P M.
                                                                                                                                                                                                                                                                                                                                                                 (GETH ) GENENTECH INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BAKER K P.
FERRARA N.
Query Match
Best Local Similarity
RESULT 52
                                                                                                                            Ouery Match
Best Local Similarity
RESULT 53
                                                                                                                                                                                                                                                              Best Local Similarity RESULT 54
                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
RESULT 55
                                                  AAB53087 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GODDARD A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (WILL/) WILLIAMS (WOOD/) WOOD W I.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Human PRO322.
WO200109327-A2.
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(GERB/)
(GERR/)
(GODD/)
(GODO/)
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(MARS/)
(PANJ/)
(PAON/)
(STEP/)
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RESULT
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Score 630.5; DB 6; Length 260; Pred. No. 1.1e-40;
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                                                                                                                                                            DB 6; Length 260;
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                               Length 260;
                                                                                                                                                                                                ABU72252 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2002192706-A1.
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9
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Human secreted and transmembrane PRO polypeptide
US200217553-A1.
28-NOV-2002.
(GETH ) GENENTECH INC.
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9
                                                                                                                                                                                                                                                                                         45.9%; Score 630.5; DB 6; 50.2%; Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Human secreted/transmembrane protein (PRO) #198.
US2003036179-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABU59848 standard; protein; 260 AA.
Novel secreted and transmembrane protein PRO322.
US2003017563-A1.
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
                              Score 630.5; DB 6
Pred. No. 1.1e-40;
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50.2%; Pred. No. 1.1e-40;
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                                                                                                                                                                                                                                                                                                                                       ADA05702 standard; protein; 260 AA. Human NOV11h protein SEQ ID NO:62. WQ2003029424.A2. IO-APR-2003. (CURA-) CURAGEN CORP.
                                                                             ABU81067 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003004311-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABU66767 standard; protein; 260 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABU61130 standard; protein; 260 AA
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RESULT 66
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Best Local Similarity 50.2%;
RESULT 65
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US2003036180-A1.
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US2002169284-A1.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
13-MAR-2003.
(GETH ) GENENTECH INC.
                                                                                                                             02-JAN-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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2002.
2003.
2007.
2007.
2007.
ESULT 67
ID ABO25038 stand?
DE Human secr.
PN US20030.
PD 20.
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Best Local Similarity
RESULT 64
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Best Local Similarity
RESULT 68
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Best Local Similarity
RESULT 61
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                                           Best Local Similarity RESULT 60
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Human PRO polypeptide #198.
10-2003068795-A1.
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08-MAY-^^^
                                                                                                                                                                                                                                                                                                                                                                        ADB30576 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003068794-A1.
                                                                                                            ADA47774 standard; protein; 260 AA. Human PRO polypeptide #198. US2003073215-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADA97084 standard; protein; 260 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADA79388 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003082763-A1.
                                                                 45.9%;
                                                                                                                                                                                             45.9%;
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RESULT 83
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 Human PRO polypeptide #198.
US2003087350-A1.
08-MAY-2003.
(GETH ) GENENTECH INC.
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US2003082705-A1.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                                                                             17-APR-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                             Best Local Similarity RESULT 78
                                                                                                                                                                                                         Best Local Similarity RESULT 79
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Best Local Similarity
RESULT 80
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Best Local Similarity
RESULT 84
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                                                                                  6; Length 260;
                                                                                                                                                                                                                                                                                                                                            DB 6; Length 260;
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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                                                                                                                            ABU67043 standard; protein; 260 AA.
Human secreted/transmembrane, PRO, protein SEQ ID 396.
US2003032155-A1.
                                                                                                                                                                                                                                                      Ap45915 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003022328-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADB19404 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003068796-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADA86424 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003082711-A1.
                                                                                                                                                                                                                                                              Learn Protein P.

Learn Match
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
ID ADA76346 standard; protein; 260 AA.
DE Human PRO polypeptide #198
PD 17-APR-200.
                                                                                                                                                                                                            Score 630.5; DB 6;
Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
ABU80399 standard; protein; 260 AA.
Human secreted/transmembrane protein PRO322.
US2003004102-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADA18996 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003054517-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADB27945 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003082704-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADA61619 standard; protein; 260 AA
                                                                              45.9%;
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50.2%;
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RESULT 75
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                                                02-JAN-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 70
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Best Local Similarity
RESULT 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity RESULT 77
                                                                                          Best Local Similarity RESULT 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
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US2003049816-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                Query Match
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RESULT 72

RESULT 73

ABREE

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Score 630.5; DB 6; Length 260; Pred. No. 1.1e-40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 45.9%; Score 630.5; DB 6; Length 260; Best Local Similarity 50.2%; Pred. No. 1.1e-40; RESULT 85
  Length 260;
                                                                                                                                                                                                                                                                                                                                                                                        Length 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 630.5; DB 6; Length 260;
Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Length 260;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADA85872 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADAB7527 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003087345-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADA91821 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
Score 630.5; DB 6;
Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Query Match 45.9%; Score 630.5; DB 6; Length 260; Best Local Similarity 50.2%; Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADABE320 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003082695-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADA84768 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322
US2003082708-A1.
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Pred. No. 1.1e-40;
                 Query Match 45.9%; Score 630.5; DB 6;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45.9%; Score 630.5; DB 6; 50.2%; Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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pred. No. 1.1e-40;
                                                                                                                                                   Score 630.5; DB 6;
Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                               Score 630.5; DB 6
Pred. No. 1.1e-40;
                                                                                                                                                                                     Human PRO polypeptide SEQ ID NO 396 (922003077713-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADA75794 standard; protein; 260 AA. Human PRO polypeptide #198. US2003082703-A1. 01-MAY-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                Human PRO polypeptide #198.
17-App-200307316-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADB30024 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003073214-Al.
                                                                      ADA74522 standard, protein, 260 AA. Human PRO polypeptide #198. US2003068798-A1. 10-APR-2003. (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                   ADA82279 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003082701-A1.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      260 AA
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RESULT 101
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
20-MAR-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                             GENENTECH INC.
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Best Local Similarity
RESULT 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
RESULT 100
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                                                                                                                                                              Best Local Similarity RESULT 97
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A (GETH ) GENE
Query Match
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                                                                                                                                                                                                                                                                                                                          Length Match

Best Local Similarity 50.2%; Score 630.5; DB 6; Length 260;

RESULT 90

DD Human PRO polypeptide #198.

PD 24-APR-2002

PA (CCC)

PD 24-APR-2002
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                                              Length 260;
                                                                                                                                                                      DB 6; Length 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADB19956 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003082691-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABO41346 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322
US2003044945-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABO19701 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322
US2003050240-A1.
                                                                                                                                                                                                                   ADA24934 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US200305521-A1.
                                           Score 630.5; DB 6;
Pred. No. 1.1e-40;
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Human secreted/transmembrane polypeptide PRO322.
US2003055216-A1.
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50.2%; Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
                                                                                                                                                                      45.9%; Score 630.5; DB 6 50.2%; Pred. No. 1.1e-40;
                                                                                           ADB14884 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003087351-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADBI3268 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003082710-A1.
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50.2%;
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Best Local Similarity 50.2%;
RESULT 92
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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L.H.) GENENTECH 1.

Lary Match
Best Local Similarity to RESULT 89
ID ADB18845 stand**
DE Novel humar
PN US2003^*
PD 17.
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21H J GENENTECH 1
2ry Match
Best Local Similarity RESULT 91
D ADB19956 standar
DD Novel humar
PN US2003°
PD 01-
                    01-MAY-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity RESULT 93
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                                                Query Match
Best Local Similarity
RESULT 87
    US2003082694-A1.
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Length 260;

Length 260;

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Length 260;

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Length 260;

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DB 6; Length 260;
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 Length 260;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABO19592 standard; protein; 260 AA.
Novel human secreted and transmembrane polypeptide #60.
US2003049633-A1.
                                                                                                                                                                                                                                                                                                                 ADB21774 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003082765-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADA88079 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003082700-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel, human secreted and transmembrane protein PRO322.
US203054516-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AURASE 16 Standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US203082709-A1.
                                                                                                                                   Score 630.5; DB 6;
Pred. No. 1.1e-40;
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Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 120
Score 630.5; DB 6;
Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                 45.9%; Score 630.5; DB 6 50.2%; Pred. No. 1.1e-40;
                                                                                                                                                                                ADB26289 standard, protein, 260 AA.
Human PRO polypeptide #198.
US2003082760-A1.
                                                  protein; 260 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADA77553 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003068797-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 119
TO ADB18293 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003077710-A1.
 45.9%;
                                                                                                                                 45.9%;
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50.2%;
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RESULT 122
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Best Local Similarity 50.2%;
                                              ADA55980 standard; protein,
Human PRO polypeptide #198
US2003003255-A1.
01-MAY-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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RESULT 121
ID ADA88079 standard, p:
DE Novel human secreted
PN US2003082700-A1.
PD 01-MAY-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity RESULT 118
 Query Match
Best Local Similarity
RESULT 114
                                                                                                                                                                                                                                                                             Best Local Similarity RESULT 116
                                                                                                                                        Best Local Similarity
RESULT 115
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Best Local Similarity
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Best Local Si
RESULT 117
                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                       Best Local Similarity 50.2%; Score 630.5; DB 6; Length 260; RESULT 108

ID ADB26841 standard; protein; 260 AA.

PN US203092147-A1.

PA '....
                                                                                                                                               Score 630.5; DB 6; Length 260; Pred. No. 1.1e-40;
                 45.9%; Score 630.5; DB 6; Length 260; 50.2%; Pred. No. 1.1e-40;
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Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 630.5; DB 6
Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 45.9%; Score 630.5; DB 6
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 630.5; DB 6
Pred. No. 1.1e-40;
                                                                                                                                             Query Match
Best Local Similarity 50.2%; Pred. N
RESULT 106
ID ADB25315 standard; protein; 260 AA.
DB Human PRO polypeptide SEQ ID NO 396.
PN US2003077715-A1.
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US2003096386-A1.
                                                              ADA47019 standard, protein, 260 AA.
Human PRO polypeptide #198.
US2003073210-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADA96332 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003082690-A1.
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Human PRO polypeptide #198.
US2003082702-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADA61056 standard; protein; 260 AA
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50.2%;
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(GETH ) GENENTECH INC.
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J5-A1.
JTH ) GENENTECH II
JETY MATCH
BEST LOCAL SIMILATITY 5
RESULT 107
ID ADA93491 stand?
DE Human PRO r
PD 24.
PA 24.
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(GETH ) GENENTECH INC.
(GETH ) GENENTECH INC.
                                                                                                            17-APR-2003.
(GETH ) GENENTECH INC
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC
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                         Best Local Similarity RESULT 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
US2003049817-A1.
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                 Query Match
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Length 260;

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PA (GETH ) GENENTECH INC.

Query Match

Query Match

45.9%; Score 630.5; DB 7; Length 260;

Best Local Similarity 50.2%; Pred. No. 1.1e-40;

RESULT 134

ID ADB15436 standard; protein; 260 AA.

DB Human PRO polypeptide #198.

PM US2003087352-A1.

PA (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     uuery Match
45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 630.5; DB 7; Length 260; Pred. No. 1.1e-40;
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Novel human secreted and transmembrane protein PRO322.
US2003082764-A1.
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Novel human secreted and transmembrane protein PRO322.
US200308269-A1.
01-MAY-2003.
                                                                                                                                                        ADA92373 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322
US2003082712-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADB38136 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003087347-A1.
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                                                                          Score 630.5; DB 7;
Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 630.5; DB 7;
Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 45.9%; Score 630.5; DB 7
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 135
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Pred. No. 1.1e-40;
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W02002102235-A2.
27-DEC-2002.
(BOSB-) BOS BIOTECHNOLOGY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADB89688 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003082698-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADB90420 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003082762-A1.
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PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 50.2%;
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Local Similarity 50.2%;
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(GETH ) GENENTECH INC.
US2003077712-A1.
24-APR-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity RESULT 138
                                                                                                Best Local Similarity RESULT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADB80561 standard;
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(GETH ) GEN
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Best Local Si
RESULT 139
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                                                                                Query Match
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Best Local Similarity 50.2%; Score 630.5; DB 7; Length 260;

RESULT 127

ID ADA97636 standard; protein; 260 AA.

PN US2003082686-A1.

PA O1-MAY-2007
     Leary Match 45.9%; Score 630.5; DB 7; Length 260; Best Local Similarity 50.2%; Pred. No. 1.1e-40; RESULT 124 Bast Local Similarity 50.2%; Pred. No. 1.1e-40; DE Human PRO polypeptide #198. PD US2003082706-A1. PD US2003082706-A1. PD PD 01-MAY-2001
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Novel human secreted and transmembrane protein PRO322.
US2003087344-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 7;
                                                                                                                                                                                                                                                                                                                                                                       Score 630.5; DB 7
Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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  RESULT 123

ID ADB28497 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADA77001 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003059909-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADB27393 standard; protein; 260 AA.
Human PRO polypeptide #198.
10/22003022239-Al.
30-JAN-2003.
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Human PRO polypeptide #198.
US2003068793-A1.
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ID ADB22878 standard, protein, 260 AA.
DE Human PRO polypeptide #198.
PN US2003077711-A1.
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Best Local Similarity 50.2%;
RESULT 126
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 132
ID ADB23651
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Best Local Similarity
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Best Local Similarity
RESULT 130
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RESULT 128
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PD
PA
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Length 260;

Length 260;

Length 260;

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Length 260;

DB 7; Length 260;

Length 260;

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vuery Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45.9%; Score 630.5; DB 7; Length 260; 50.2%; Pred. No. 1.1e-40;
                                                                                                                                                                                                                                            ADB46564 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US20031082692-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 45.9%; Score 630.5; DB 7; Best Local Similarity 50.2%; Pred. No. 1.1e-40; RESULT 155
                         45.9%; Score 630.5; DB 7; 50.2%; Pred. No. 1.1e-40;
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                                                                                                                                                                                                                                                                                                                                               Score 630.5; DB 7;
Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 630.5; DB 7;
Pred. No. 1.1e-40;
                                                                                                                                                    CSTART COURTECH INC. (GETH) GENERITECH INC. 15.9%; Score 630.5; DB 7. 17.4 Match 15.0%; Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45.9%; Score 630.5; DB 7 50.2%; Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                     ADC44043 standard; protein; 260 AA.
Human secreted/transmembrane protein, PRO322.
US2003054986-A1.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADC61803 standard; protein; 260 AA.
Human secreted/transmembrane protein, PRO322.
US2003049684-A1.
JaARA-2003.
(GETH.) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADC66867 standard; protein; 260 AA.
Human secreted/transmembrane protein, PRO322.
US2003060406-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADC68991 standard; protein; 260 AA.
Human secreted/transmembrane protein, PRO322.
US2003064407-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADC63051 standard; protein; 260 AA.
Human secreted/transmembrane protein, PRO322.
US2003068648-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human secreted/transmembrane protein, PRO322. US2003069178-A1.
                                                                                 ADB36169 standard; protein; 260 AA.
Human PRO polypeptide SEQ ID NO 396.
US2003077720-Al.
24-APR-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADC68116 standard; protein; 260 AA.
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50.2%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
      (GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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                                                                                                                                                                                                  Best Local Similarity RESULT 152
                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
RESULT 153
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Best Local Similarity
RESULT 156
                       Query Match
Best Local Similarity
RESULT 151
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RESULT 158
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                                         45.9%; Score 630.5; DB 7; Length 260; 50.2%; Pred. No. 1.1e-40;
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Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 144
                                                                                                                                                                                                      DB 7; Length 260;
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Pred. No. 1.1e-40;
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                                                                                                                                                                                                                                                             ADB47144 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003082687-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADB77356 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003082696-A1.
                                                                                                                                                                                                  45.9%; Score 630.5; DB 7 50.2%; Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Human PRO polypeptide SEQ ID NO 396.
US2003077719-A1.
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US2003077718-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADB34513 standard, protein, 260 AA. Human PRO polypeptide SEQ ID NO 396. US2003077717-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADB33961 standard; protein; 260 AA. Human PRO polypeptide SEQ ID NO 396. US2003077716-A1.
                                                                                              ADB73901 standard; protein; 260 AA.
Human PRO polypeptide #60.
US2003045462-A1.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                          ADB86751 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003082697-A1.
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Human PRO polypeptide #60.
US2003083248-A1.
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Best Local Similarity 50.2%;
RESULT 145
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Query Match
Best Local Similarity
RESULT 142
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Best Local Similarity
RESULT 146
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Best Local Similarity
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Length 260;

Length 260;

Length 260;

Length 260;

DB 7;

50.2%; Pred. No. 1.1e-40;

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D. ADG7324 standard; protein; 260 AA.

E. Novel human secreted and transmembrane protein Seq ID396.

N. US2003087366-A1.

D. OB-MAY-2003.

A. (GETH ) GENENTECH INC.

Query Match

45.9%; Score 630.5; DB 7; Length 260;
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Score 630.5; DB 7; Length 260;
Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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                                                                                                                             Length 260;
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Novel human secreted and transmembrane protein Seg ID396.
US2003087365-A1.
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Novel human secreted and transmembrane protein PRO322.
US2003092105-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADC50437 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003092106-A1.
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Novel human secreted and transmembrane protein PRO322.
US2003092107-A1.
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
                                                                                                                                                                              ADC67491 standard; protein; 260 AA.
Human secreted/transmembrane protein, PRO322.
US2003073131-A1.
                                                                                                                                                                                                                                                                                                         ADC62427 standard; protein; 260 AA.
Human secreted/transmembrane protein, PRO322.
US2003073624-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                    ADC42060 standard; protein; 260 AA.
Human secreted/transmembrane protein, PRO322.
US2003104998-A1.
                                              ADC41436 standard; protein; 260 AA.
Human secreted/transmembrane protein, PRO322.
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(GETH ) GENENTECH IN

QUEYY MATCH

BEST LOCAL SIMILATITY 5

RESULT 166

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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 162
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Best Local Similarity
RESULT 168
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Best Local Similarity
RESULT 167
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RESULT 164
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   Query Match
Best Local Similarity
                                                                                   US2003072745-A1.
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Length 260;
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Novel human secreted and transmembrane protein Seg ID396.
US2003087364-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADC59099 standard; protein; 260 AA.

Novel human secreted and transmembrane protein Seq ID396.
US2003339-A1.
(98-MAY-2003.
(GETH ) GENENTECH INC.
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Novel human secreted and transmembrane protein Seg ID396.
US2003087363-A1.
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Novel human secreted and transmembrane protein Seg ID396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADD03221 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322
                                   ADC60515 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003087367-A1.
                                                                                                                                                                  ADC50990 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322
US2003087361-A1.
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Best Local Similarity 50.2%; Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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50.2%; Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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US2003087362-A1.
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08-MAY-2003.
(GETH ) GENENTECH INC.
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RESULT 175
                                                                                                                       45.9%;
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(GETH ) GENENTECH INC.
                                                                                     08-MAY-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity RESULT 169
                                                                                                                       Query Match
Best Local Similarity
RESULT 170
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RESULT 171
ID ADC65517 standard;
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RESULT 172
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ADC47969 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003194771-A1.
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                                                                                                        Score 630.5; DB 7; Length 260;
Pred. No. 1.1e-40;
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                 ADC90213 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003087348-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADD04625 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003087354-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADC80581 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003092103-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 7;
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                                                                                                                                                                                                                                                       45.9%; Score 630.5; DB 7 50.2%; Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Human kallikrein 8 protein SEQ ID NO:2.
WO2003085404-A1.
                                                                                                                                                            ADC69632 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003194770-A1.
                                                                                                                                                                                                                                                                                                        ADC48521 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003194773-A1.
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Human PRO polypeptide #198.
US2003194776-A1.
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Human PRO polypeptide #198.
US2003194774-A1.
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                                                                                                         45.9%;
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Best Local Similarity 50.2%;
RESULT 186
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity 5.
RESULT 180
ID ADC46521 stand**
DB Human PRO r
PN US20031*
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC
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RESULT 185
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Best Local Similarity
RESULT 187
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Best Local S
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RESULT 178
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Score 630.5; DB 7; Length 260; Pred. No. 1.1e-40;
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                                       7; Length 260;
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                                                                                          ADC80029 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003087358-A1.
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Novel human secreted and transmembrane protein PRO322.
US2003203438-A1.
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Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45.9%; Score 630.5; DB 7; 50.2%; Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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ID ADD11321 standard; protein; 260 AA.
DE Human secreted/transmembrane PRO polypeptide #36
N US2003105013-A1.
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Human secreted/transmembrane PRO polypeptide #36.
US2003105012-A1.
                                     Score 630.5; DB 7
Pred. No. 1.1e-40;
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Human PRO polypeptide #198.
US2003194775-A1.
16-OCT-2003.
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Human PRO polypeptide #198.
US2003194769-A1.
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Human PRO polypeptide #198.
US2003194792-A1.
16-OCT-2003.
(GETH) GENENTECH INC.
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Best Local Similarity 50.2%;
RESULT 192
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Best Local Similarity 50.2%;
RESULT 188
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Local Similarity 50.2%;
16-OCT-2003.
(GETH ) GENENTECH INC.
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Juery Match
Best Local Similarity RESULT 195
ID ADD37114 stander
PN US20031
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ID ADD53090 standard;
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Query Match
Best Local Similarity 50.2%;
RESULT 213
ID ADD91978 standard; protein;
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50.2%;
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Local Similarity 50.2%;
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Human PRO polypeptide #198.
US2003194772-A1.
                                                                               45.9%;
                                                                                                        50.2%;
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Human PRO polypeptide #198.
US2003203428-Al.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC
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Best Local Similarity
RESULT 209
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Best Local Similarity
RESULT 207
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                                                                                                                                                                                                                                                                                                        Score 630.5; DB 7; Length 260; Pred. No. 1.1e-40;
                                                                                                                Length 260;
              Human tumour antigen derived gene-14 (TADG-14) protein. US2002037581-A1. 28-MAR-2002. (UABR-) UAB RES FOUND.
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Novel human secreted and transmembrane protein PRO322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADD54213 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003203432-A1.
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 630.5; DB 7 Pred. No. 1.1e-40;
                                                                                                                     Score 630.5; DB 7
Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human secreted/transmembrane protein, PRO322. US2003096744-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADD91426 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003199055-A1.
CGETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADD92530 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003199030-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  260 AA
                                                                                                                                                                         Human PRO polypeptide #198.
16-Orm-2003
                                                                                                                                                                                                                                                                                                                                                                              ADD02597 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003203431-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADD02031 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003203430-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADE49429 standard; protein; 260 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45.9%;
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Best Local Similarity 50.2%;
RESULT 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45.9%;
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50.2%;
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Human PRO polypeptide #198.
US2003199057-A1.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 50.2%;
RESULT 198
                                                                                                                     45.9%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-OCT-2003.
(GETH ) GENENTECH INC.
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LOG3.

LAT MATCH

BEST LOCAL SIMILARITY P.

RESULT 199

ID ADD02031 stand**

DB Human PRO r.

PN US2003**

PD 30-*

PA
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RESULT 201
ID ADE49429 standard; pr
DE Human secreted/transm
PN US2003096744-Al.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                      16-OCT-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GETH ) GENENTECH INC
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Best Local Similarity
RESULT 197
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Best Local Similarity
RESULT 200
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Score 630.5; DB 7; Length 260; Pred. No. 1.1e-40;
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                                                                                                                                                                                                                                                                                                               Score 630.5; DB 7; Length 260; Pred. No. 1.1e-40;
                                                                                                                                                          Score 630.5; DB 7; Length 260; Pred. No. 1.1e-40;
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Length 260;
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Novel human secreted and transmembrane protein PRO322.
US2003194767-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 45.9%; Score 630.5; DB 7;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
    DB 7;
    Score 630.5; DB 7 Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADE16597 standard; protein; 260 AA.
Human secreted/transmembrane protein, PRO322.
US2003203435-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADD73212 standard; protein; 260 AA.
ADD73212 standard; protein; PRO322.
US2003203436-Al.
                                                                                                                                                                                                                                                                                                                                                                            ADB35483 standard; protein; 260 AA.
Human secreted/transmembrane protein, PRO322.
US2003203434-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human PRO polypeptide #198.
(052003199053-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 212
ID ADE17846 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      260 AA
                                                             ADE22269 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003199056-A1.
                                                                                                                                                                                                                        260 AA
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vuery Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 45.9%; Score 630.5; DB 7; Length 260; Best Local Similarity 50.2%; Pred. No. 1.1e-40; RESULT 230
          Query Match 45.9%; Score 630.5; DB 7; Length 260; Best Local Similarity 50.2%; Pred. No. 1.1e-40; RESULT 224
                                                                                                                                               Score 630.5; DB 7; Length 260; Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                              Query Match 45.9%; Score 630.5; DB 7; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 630.5; DB 7; Length 260; Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
                                                                                                                                                                                              ADE32889 standard; protein; 260 AA.

Novel human secreted and transmembrane protein PRO322.
US2003194766-A1.
16-OCT-2003.
(GETH ) GENENTECH INC.
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Human secreted/transmembrane protein, PRO322.
US2003203433-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Auman PRO polypeptide #198.
US2003199031-A1.
23-OCT-2003.
(GETH ) GENENTECH INC.
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US2003194777-A1.
16-OCT-2003.
(GETH ) GENENTECH INC.
                                                              ADD78939 standard, protein; 260 AA.
Human PRO polypeptide #198.
US2003203429-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human PRO polypeptide #198.
US2003207418-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADD89625 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003199028 A1.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                               ADE42581 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003199032-A1.
23-OCT-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADE04708 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003199034-AA.
C3-OCT--2003.
(GETH ) GENENTECH INC.
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                                                                                                                                              Query Match
Best Local Similarity 50.2%;
RESULT 225
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Best Local Similarity 50.2%;
RESULT 228
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RESULT 229
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Best Local Similarity 50.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-OCT-2003.
(GETH ) GENENTECH INC.
                                                                                                              30-OCT-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
 (GETH ) GENENTECH INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                 vuery Match
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 216
                                Score 630.5; DB 7; Length 260;
Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                 Score 630.5; DB 7; Length 260;
Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 260;
                                                                            ADE33993 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US_003194791_A1.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 630.5; DB 7;
Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADD72570 standard; protein; 260 AA.
Human secreted/transmembrane protein, PRO322.
US2003194781-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADE19502 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003199025-A1.
                                                                                                                                                                                                     Human PRO polypeptide #198.
US2003207417-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADE18950 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003199026-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADE43146 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003199033-A1.
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Human PRO polypeptide #198.
US2003199059-A1.
                                                                                                                                                                                                                                                                                                                                                ADD93082 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003194768-A1.
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Human PRO polypeptide #198.
US2003199064-Al.
23-OCT-2003.
                                45.9%;
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Local Similarity 50.2%;
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Best Local Similarity 50.2%;
RESULT 219
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(GETH ) GENENTECH INC.
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LY MATCH

Best Local Similarity 5.

RESULT 20

ID ADE18950 standa*

DE Human PRO P.

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(GETH ) GENENTECH INC.
                 GENENTECH INC
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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                               Query Match
Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
RESULT 221
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16-OCT-2003
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Best Local Si
RESULT 223
                                                                                                                                                                                                                                                                                                 Query Match
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                 (GETH)
                                                                 RESULT 215
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RESULT 218
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7; Length 260;

50.2%; Pred. No. 1.1e-40;

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Best Local Similarity RESULT 242
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Novel human secreted and transmembrane protein PRO322.

Novel human secreted and transmembrane protein PRO322.

Novel human secreted and transmembrane protein PRO322.

Novel human secreted and transmembrane protein PRO322.

Novel human secreted and transmembrane protein PRO322.

Novel human secreted and transmembrane protein PRO322.
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                                                        Score 630.5; DB 7; Length 260;
Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 260;
                                                                                                                                                                                                                                              ADG21546 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003207355-A1.
                                                                                                                                                                                                                                                                                                                                                                                ADG21187 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003207384-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 7;
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
                                                                                                                                                                                             Score 630.5; DB 7
Pred. No. 1.1e-40;
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Human secreted/transmembrane protein, PRO322.
US2003206915-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADGS2992 standard; protein; 260 AA.
Human secreted/transmembrane protein, PRO322.
US2003216561-A1.
                                                                                                         ADF47235 standard; protein; 260 AA.
Human secreted/transmembrane protein, PRO322.
US2003195333-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADF97522 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003207370-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADG80034 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003207372-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADG80586 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003207373-A1.
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Best Local Similarity 50.2%;
RESULT 240
                                                             45.9%;
50.2%;
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                                                                                                                                                                                             Match 45.9%;
Local Similarity 50.2%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                          24-A1.
2003.
2.H ) GENENTECH II.
2ry Match
Best Local Similarity 5
RESULT 236
ID ADF97522 stand>
DE Human PRO r
PN US20037
PD 06.
Local Similarity 5
RESULT 23
ID ADF47235 stand>
DE Human secre
PN US20031
                                                                                                                                                             16-OCT-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                 06-NOV-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 241
                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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                                                                                                                                                                                                Query Match
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SEQ ID NO:500
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                                                                                         Length 260;
                                                                                                                                                                                                                                               Length 260;
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Novel human secreted and transmembrane protein PRO322.
US2003087355-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUH81407 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003207377-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADNIS975 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003087353-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADN16604 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
ADH55878 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003207379-A1.
                                                                                                                                                                                                                                                                                                       ADI64097 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003207385-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADH81959 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322
US2003207388-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADN39182 standard; protein; 260 AA.
Cancer/angiogenesis/fibrosis-related polypeptide,
WO2003042661-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45.9%; Score 630.5; DB 7; 50.2%; Pred. No. 1.1e-40;
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                                                                                           Score 630.5; DB 7;
Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 630.5; DB 7 Pred. No. 1.1e-40;
                                                                                                                                                                                                                                               45.9%; Score 630.5; DB 7 50.2%; Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                     Score 630.5; DB 7
Pred. No. 1.1e-40;
                                                                                                                                                   ADIG1072 standard; protein; 260 AA.
Human secreted/transmembrane protein, PRO322.
US2003077700-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-MAY-2003.
(EOSB-) EOS BIOTECHNOLOGY INC.
                                     US2003207
06-NOV-2003.
(GETH ) GENENTECH INC.
45.9%;
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RESULT 247
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                                                                                                                             24-APR-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                     (GETH ) GENENTECH INC.
                                                                                                 Query Match
Best Local Similarity
RESULT 243
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Best Local Similarity
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Score 630.5; DB 8; Length 260; Pred. No. 1.1e-40;
                                                                                                                                                                                                                                        DB 7; Length 260;
                                                                                                                                                                                                                                                                                                                                                                         45.9%; Score 630.5; DB 7; Length 260; 50.2%; Pred. No. 1.1e-40;
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                                                                                                   Length 260;
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              ADN15423 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003087356-A1.
                                                                                                                                    AUN14871 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US203087357-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                           ADI63545 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003207387-A1.
                                                                                                                                                                                                                                                                                      ADI65046 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003207386-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADC81133 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003092115-A1.
                                                                                               Score 630.5; DB 7;
Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45.9%; Score 630.5; DB 8; 50.2%; Pred. No. 1.1e-40;
                                                                                                                                                                                                                                    45.9%; Score 630.5; DB 7 50.2%; Pred. No. 1.1e-40;
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Human PRO polypeptide #198.
US2003092113-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADD86349 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003203440-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADB75797 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003211571-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADD76581 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003100087-A1.
                                              US200300...
08-MAY-2003.
(GETH ) GENENTECH INC.
45.9%;
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Local Similarity 50.2%;
                        ... Becl.
... d7356-A1.
... d7356-A1.
... (GETH ) GENENTECH II.
Query Match
BEST Local Similarity 5
RESULT 252
ID ADNI4871 stander
DE Novel humar
PN US20030"
PD 08-"
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                        (GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                                                                                                                    08-MAY-2003.
(GETH ) GENENTECH INC
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Best Local Similarity
                                                                                                                                                                                                                                                 Best Local Similarity RESULT 253
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Best Local Similarity
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Best Local Similarity
RESULT 260
                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
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RESULT 251
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Query Match 45.9%; Score 630.5; DB 8; Length 260;
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 267
                                                                                                                                                                8; Length 260;
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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                                                                                                                                                                                                                                                                                                                                                                                                               Score 630.5; DB 8;
Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 630.5; DB 8;
Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                  ADE41322 standard; protein; 260 AA.
Human secreted/transmembrane PRO polypeptide #36
US2003100497-A1.
                                                                                                                                                                Score 630.5; DB 8 Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 630.5; DB 8 Pred. No. 1.1e-40;
ADB48729 standard; protein; 260 AA.
Human secreted/transmembrane protein, PRO322.
US2003104536-A1.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADE23373 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003092108-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human PRO polypeptide #198.
US2003092110-A1.
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Human PRO polypeptide #198.
US2003199054-A1.
23-OCT-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADE24568 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003092111-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADD87393 standard, protein, 260 AA.
Human PRO polypeptide #198.
US2003203439-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADE89830 standard; protein; 260 AA.
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Human PRO polypeptide #198.
US2003199062-A1.
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                                                                                                                                                             45.9%;
50.2%;
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RESULT 265
                                                                                                                                                                                                                                                                                                                                                                                                               45.9%;
50.2%;
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Local Similarity 50.2%;
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RESULT 269
ID ADE89830 ct...
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Human PRO polypeptide #198.
US200319474A1.
16-OCT--2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                 29-MAY-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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RESULT 262
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RESULT 266
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Best Local S
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ADE95279 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003199052-A1.
C3-OCT-2003.
(GETH ) GENENTECH INC.
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RESULT 281
                                                                                                                                                                      45.9%;
                                                                Query Match 45.9%;
Best Local Similarity 50.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-OCT-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
RESULT 283
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                                                                                                                                                                             Best Local Similarity RESULT 277
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                                                                                                                                                                         Query Match
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Pred. No. 1.1e-40;
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Human secreted/transmembrane protein, PRO322.
US2003198994-A1.
    Juman secreted/transmembrane protein, PRO322.
                                                                                                                                                                                                                                                                                                                                                                                                                                 ADF61470 standard; protein; 260 AA.
Human secreted/transmembrane protein, PRO322.
US2003195345-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADF45958 standard; protein; 260 AA.
Human secreted/transmembrane protein, PRO322.
US2003195148-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADE94727 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003199027-A1.
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Human PRO polypeptide #198.
US2003199061-A1.
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RESULT 273
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Best Local Similarity 50.2%;
RESULT 274
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                           ASHKENAZI A J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GETH ) GENENTECH INC
                                                      BAKER K P.
BOTSTEIN D.
DESNOYERS L.
                                                                                                                                                                                                                                                                                                                                                       (TUMA/) TUMAS D.
(WILL/) WILLIAMS P M.
(WOOD/) WOOD W I.
                                                                                              EATON D L.
FERRARA N.
FILVAROFF E.
                                                                                                                                                                                                 GODOWSKI P J. GIRMALDI J C.
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HILLIAN K J.
KUJAVIN I J.
KUO S S.
NAPTER M A.
PAN J.
PAN J.
SHELTON D L.
STEWART T A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
RESULT 272
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RESULT 275
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                                                                                                                                                          GERBER H.
                 JS2003130181-A1.
                                                                                                                                    FONG S.
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(BAKE/)
(BOTS/)
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(ROYM/)
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45.9%; Score 630.5; DB 8; Length 260; 50.2%; Pred. No. 1.1e-40;
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Score 630.5; DB 8; Length 260; Pred. No. 1.1e-40;
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PA (GETH ) GENENTECH INC.

Query Match 45.9%; Score 630.5; DB 8;

Best Local Similarity 50.2%; Pred. No. 1.1e-40;

RESULT 278
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Best Local Similarity 50.2%; Score 630.5; DB 8;
RESULT 282
ID APEZATBO standard; protein; 260 AA.
DE Human secreted/transmembrane protein, PR0322.
PN US2003199436-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
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Pred. No. 1.1e-40;
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Human secreted/transmembrane protein, PRO322.
US2003199437-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                       ADF40786 standard; protein; 260 AA.
Human secreted/transmembrane protein, PR0322.
US2003199021. A1.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADF23730 standard; protein; 260 AA.
Human secreted/transmembrane protein, PRO322.
US2003203402-A1.
(GETH ) GENENTECH INC.
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Human secreted/transmembrane protein, PRO322.
US2003194780-A1.
                                                                                                                                                                                                                                             ADF24354 standard; protein; 260 AA.
Human secreted/transmembrane protein, PRO322.
US2003204055-A1.
                                     RESULT 276
ID ADE93389 standard; protein; 260 AA.
DE Human PRO polypeptide #198.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADF34970 standard; protein; 260 AA. Human PRO polypeptide #198. US20031990929-AA. 23-OCT-2003. (GETH ) GENENTECH INC.
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US2003207352-A1.
                                                                    DB 8; Length 260;
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Novel human secreted and transmembrane protein PRO322.
US2003199051-A1.
23-OCT-2003.
(GETH ) GENENTECH INC.
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Novel human secreted and transmembrane protein PRO322.
US2003199058-A1.
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Human secreted/transmembrane protein, PRO322.
US2003199435-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADF25455 standard; protein; 260 AA.
Human secreted/transmembrane protein, PR0322.
US2003211092-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADF26556 standard; protein; 260 AA.
Human secreted/transmembrane protein, PRO322.
US2003199674-A1.
                                                                                                                                                                                                                                                                                                                                                                                         ADF33089 standard; protein; 260 AA.
Human secreted/transmembrane protein, PRO322.
US2003211091-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADF34145 standard; protein; 260 AA.
Human secreted/transmembrane protein, PRO322.
US2003194410-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADF46582 standard; protein; 260 AA.
Human secreted/transmembrane protein, PRO322.
US2003195344-A1.
                                                                                                         Human PRO polypeptide #198.
US2003199063-Al.
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23-OCT-2003.
(GETH ) GENENTECH INC.
45.9%; SC
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
RESULT 287
ID ADP33089 standard; pr
DE Human secreted/transm
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC
                                                                                                                                                                                                     Query Match
Best Local Similarity
RESULT 286
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                                                      Query Match
Best Local Similarity
RESULT 285
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RESULT 291
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RESULT 289
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Query Match 45.9%; Score 630.5; DB 8; Length 260; Best Local Similarity 50.2%; Pred. No. 1.1e-40; RESULT 300
                                                                                                                                           vuery Match 45.9%; Score 630.5; DB 8; Length 260; Best Local Similarity 50.2%; Pred. No. 1.1e-40; RESULT 295
                                                                                                                                                                                                                                                                                                          Score 630.5; DB 8; Length 260; Pred. No. 1.1e-40;
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                DB 8; Length 260;
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Pred. No. 1.1e-40;
                                                                ADG22098 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322
US2003207360-A1.
(GEVNV-2003.
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Novel human secreted and transmembrane protein PRO322.
US2003207426-A1.
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                Score 630.5; DB 8 Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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US2003207422-A1.
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082003207353-Al.
                                                                                                                                                                                                           ADG20168 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003207376-A1.
(GETH ) GENENTECH INC.
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Human PRO polypeptide #198.
US2003208055-A1.
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Human PRO polypeptide #198.
US2003207351-A1.
(GFTH ) GENENTECH INC.
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Human PRO polypeptide #198.
US2003207359-A1.
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Human PRO polypeptide #198.
US2003207375-A1.
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Just ) GENENTECH INC.

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Best Local Similarity 50.2%; Present 299

ID ADG03476 standard; probe Human PRO polyper

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Best Local Similarity 50.2%;
RESULT 302
                                 50.2%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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RESULT 301
ID ADG16782 standard; p:
DE Human PRO polypeptide
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC
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Best Local Similarity
RESULT 297
                                 Local Similarity
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(GETH) GENENTECH INC. 06-NOV-2003 (GETH) GEN 06-NOV-200 Query Match Query Match Score 630.5; DB 8; Length 260; Pred. No. 1.1e-40; Score 630.5; DB 8; Length 260; Pred. No. 1.1e-40; Score 630.5; DB 8; Length 260; Pred. No. 1.1e-40; Length 260; Score 630.5; DB 8; Length 260; Pred. No. 1.1e-40; Score 630.5; DB 8; Length 260; Pred. No. 1.1e-40; Score 630.5; DB 8; Length 260; Pred. No. 1.1e-40; Score 630.5; DB 8; Length 260; Pred. No. 1.1e-40; Length 260; ADG23739 standard; protein; 260 AA. Novel human secreted and transmembrane protein PRO322. ADG24929 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003207427-A1.
06-NOV-2003. ADG08402 standard; protein; 260 AA. Novel human secreted and transmembrane protein PRO322 US2003207424-A1. Score 630.5; DB 8; Pred. No. 1.1e-40; Score 630.5; DB 8; Pred. No. 1.1e-40; ADG06155 standard; protein; 260 AA. Human PRO polypeptide #198. US2003207374-A1. ADG04028 standard; protein; 260 AA. Human PRO polypeptide #198. US2003207423-A1. Human PRO polypeptide #198. 022003219885-Al. ADG19508 standard; protein; 260 AA-Human PRO polypeptide #198. 1052003207425-A1. 06-NOV-2003. ADF96970 standard; protein; 260 AA. Human PRO polypeptide #198. US2003207371-A1. ADG13345 standard; protein; 260 AA 45.9%; 45.9%; 50.2%; 45.9%; 45.9%; 50.2%; 45.9%; 50.2%; 45.9%; 45.9%; 45.9%; / Match 45.9%; Local Similarity 50.2%; 50.2%; Human PRO polypeptide #198. US2003207357-A1. 06-NOV-2003. (GETH) GENENTECH INC. 27-NOV-2003. (GETH) GENENTECH INC. 06-NOV-2003. (GETH) GENENTECH INC. 06-NOV-2003. (GETH) GENENTECH INC. 06-NOV-2003. (GETH) GENENTECH INC GENENTECH INC (GETH) GENENTECH INC (GETH) GENENTECH INC (GETH) GENENTECH INC Best Local Similarity Query Match Best Local Similarity RESULT 308 Query Match Best Local Similarity RESULT 309 Best Local Similarity RESULT 306 Local Similarity Best Local Similarity RESULT 310 Best Local Similarity RESULT 304 Local Similarity US2003207389-A1. 06-NOV-2003 06-NOV-2003 06-NOV-2003 Query Match Query Match Query Match Query Match Query Match Query Match Query Match Best Loca RESULT 305 RESULT 311 BBBBB PONDE BEREE BARBER

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Length 260;
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Length 260;
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Novel human secreted and transmembrane protein PRO322.
US2003207364-A1.
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Novel human secreted and transmembrane protein PRO322.
US2003207365-A1.
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Novel human secreted and transmembrane protein PRO322.
US2003207428-A1.
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Novel human secreted and transmembrane protein PRO322.
Query Match
Best Local Similarity 50.2%; Pred. No. 1.1e-40;
BESTL 312
DE ADG7226 standard; protein; 260 AA.
DE Novel human secreted and transmembrane protein PRO322.
PN US2003207350-A1.
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Novel human secreted and transmembrane protein PRO322.
US2003207390-A1.
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Novel human secreted and transmembrane protein PRO322
US2003207356-A1.
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Novel human secreted and transmembrane protein PRO322
US2003194778-A1.
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Pred. No. 1.1e-40;
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Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 318
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Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 316
                                                                                                                                                          45.9%; Score 630.5; DB 8 50.2%; Pred. No. 1.1e-40;
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Human PRO polypeptide #198.
US2003207358-A1.
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Local Similarity 50.2%;
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Best Local Similarity 50.2%;
RESULT 317
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 314
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RESULT 313
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Match
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 RESULT 330
45.9%; Score 630.5; DB 8; Length 260; 50.2%; Pred. No. 1.1e-40;
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Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 329
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Pred. No. 1.1e-40;
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                                            ADG58585 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003207368-A1.
(GGTH) GENENTECH INC.
                                                                                                                                                                                                                                                                                                      ADGS8033 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US20320735-A1.
G6-NOV-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                         ADG70951 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003207420-A1.
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US203207415-Al.
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Novel human secreted and transmembrane protein PRO322.
US2003207421-A1.
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Novel human secreted and transmembrane protein PRO322.
US2003207419-A1.
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Pred. No. 1.1e-40;
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Human secreted/transmembrane protein, PRO322.
US2003207803-A1.
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Human PRO polypeptide #198.
US2003207805-A1.
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Human PRO polypeptide #198.
US2003077723-A1.
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50.2%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 323
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Best Local Similarity
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Best Local Similarity
RESULT 328
           Best Local Similarity RESULT 321
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RESULT 326
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Local Similarity 50.2%; Score 630.5; DB 8; Length 260;
RESULT 33.2
ID ADG52441 standard; protein; 260 AA.
PN US2003207414-A1.
PD 06-NOV-2003
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Novel human secreted and transmembrane protein PRO322.
US2003207366-A1.
06-NOV-2003.
(GETH.) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                            ADG54169 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
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Novel human secreted and transmembrane protein PRO322.
US2003207378-A1.
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Best Local Similarity 50.2%; Pred. No. 1.1e-40;
RESULT 336
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Human secreted/transmembrane protein, PRO322.
US2003216305-A1.
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Human secreted/transmembrane protein, PRO322.
US2003216560-A1.
ADG49944 standard; protein; 260 AA.
Human secreted/transmembrane protein, PRO322.
US2003215905-A1.
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Human PRO polypeptide #198.
US2003194793-A1.
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Local Similarity 50.2%;
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50.2%;
                                            PD 20-NOV-2003.

PA (GETH ) GENENTECH INC.

QUETY MATCh 45.9%;

Best Local Similarity 50.2%;

RESULT 331
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RESULT 338
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
RESULT 334
ID ADG49320 standard, pr
DE Human secreted/transm
PN US2003216305-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity RESULT 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
RESULT 335
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Best Local Similarity
RESULT 339
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Human TADG-14 protein. US6642013-B1.

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Score 630.5; DB 8; Length 260; Pred. No. 1.1e-40;
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                                                                                  Length 260;
                                                                                                                                                                                                                       Score 630.5; DB 8; Length 260; Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 260;
                                                                                                                                                                                                                                                                                                                                                                                                                ADGS9761 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003207369-A1.
(G6-NOV-2013).
(GETH ) GENENTECH INC.
ADG61489 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
VS2003207429-A1.
06-NOV-2003.
                                                                                                                                                                                                                                                                     ADG54721 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322
US2003207367-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 630.5; DB 8;
Pred. No. 1.1e-40;
                                                                                  Score 630.5; DB 8;
Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADG59136 standard; protein; 260 AA.
Human secreted/transmembrane protein, PRO322.
US2004005657-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADG62592 standard; protein; 260 AA.
Human secreted/transmembrane protein, PRO322.
US2004006219-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADG51192 standard; protein; 260 AA.
Human secreted/transmembrane protein, PRO322.
US2004005312-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADH43505 standard; protein; 260 AA.
Human PRO polypeptide #36.
US2003224984-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADI39730 standard; protein; 260 AA
                                                                                                                                      ADH28576 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2003022331-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           260 AA
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Best Local Similarity 50.2%;
RESULT 348
ID ADI39730 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human PRO polypeptide #198. US2003207361-Al.
                                                                                    45.9%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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                                                                    (GETH ) GENENTECH INC
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 344
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RESULT 347
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Best Local Similarity
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Best Local Similarity
RESULT 346
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Best Local Si
RESULT 341
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ADH25617 standard; protein; 260 AA.
Human neurotrimin homologue related protein sequence SEQ ID NO:395.
EP1386931-A1.
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Best Local Similarity 50.2%; Pred. No. 1.1e-40;
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Novel human secreted and transmembrane protein PRO322.
US2004039164-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADI18326 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322
US2003207349-A1.
0G-NOV-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGG9276 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2004009547-A1.
(GETH ) GENENTECH INC.
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Novel human secreted and transmembrane protein PRO322.
US2003207383-A1.
                                                                                                                                                                                                                                                                  ADG09928 standard; protein; 260 AA.

Novel human secreted and transmembrane protein PRO322.
US2004009548-Al.
15-JAN-2004.
(GETH) GENENTECH INC.
ery Match
ery Match
Similarity 50.2%; pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                               ADI15399 standard; protein; 260 AA.
Novel human secreted and transmembrane protein PRO322.
US2003207382-A1.
04-NOV-2003.
(UYAR-) UNIV ARKANSAS MEDICAL SCI.
ery Match
ery Match 50.2%; Pred. No. 1.1e-40;
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PA (GETH ) GENENTECH INC.

Query Match

45.9%; Score 630.5; DB 8;

Query Match

15.0%; Pred. No. 1.1e-40;

RESULT 352
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Pred. No. 1.1e-40;
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Human PRO polypeptide #198.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADI37154 standard; protein; 260 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 50.2%;
RESULT 357
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RESULT 356
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Best Local Similarity 50.2%;
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(UYAR-) UNIV ARKANSAS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human TADG-14 protein.
US2003199010-A1.
                                                                                                                                                                   04-FEB-2004.
(GETH ) GENENTECH INC.
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                                            Query Match
Best Local Similarity
RESULT 349
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(GETH ) GEN
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RESULT 354
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ANDERSON D W.

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Score 630.5; DB 8; Length 260; Pred. No. 1.1e-40;
                                     Length 260;
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                                     45.9%; Score 630.5; DB 8; 50.2%; Pred. No. 1.1e-40;
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11-MAR-2004.

(GETH ) GENENTECH INC.

(GETY Match 45.9%; Score 630.5; DB 8

lery Match 50.2%; Pred. No. 1.1e-40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADL07228 standard; protein; 260 AA.
Human secreted/transmembrane protein, PRO322.
US2004063921-A1.
                                                                                                                                                                                                                                                                                                                                                                                   ADM17394 standard; protein; 260 AA.
Human secreted/transmembrane protein, PRO322.
US2004048332-A1.
                                                                      ADK82850 standard; protein; 260 AA. Human PRO polypeptide #36. US2004043927-AI. GA-MAR-2004. (GETH.) GENENTECH INC.
                                                                                                                                                                           ADJ65624 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2004038335-A1.
                                                                                                                                                                                                                                                                                 ADM27760 standard; protein; 260 AA.
Human PRO polypeptide #198.
US2004048333-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADM42484 standard, protein; 260 AA.
Human PRO polypeptide #198.
US2004058424-A1.
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50.2%;
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Best Local Similarity 50.2%;
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GUO X.
GUO X.
PATTURAJAN M.
SPYTEK K A.
EDINGER S R.
ELIERMAN K.
MALYANKAR U M.
                                                                                                                                                                                                                 26-FEB-2004.
(GETH ) GENENTECH INC.
            26-FEB-2004.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORT T.
GORMAN L.
ZERHUSEN B D.
                                                                                                                                                                                                                                            Query Match
Best Local Similarity
RESULT 360
                                              Best Local Similarity RESULT 358
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Best Local Similarity
RESULT 361
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RESULT 362
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MILLET I.
PEYMAN J A.
KEKUDA R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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US2004038223-A1.
US2004038336-A1.
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Best Local Si
RESULT 364
                                  Query Match
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RESULT 363
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Human ovarian cancer-related tumour marker kallikrein 8 (hK8) protein.
WO2004075713-A2.
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WHEN MATCH

45.94; Score 630.5; DB 8; Length 260;

BESULT 367

ID AD195828 standard; protein; 260 AA.

PB Human PRO Polypeptide #198.

PD 24.APR-2003

PA (COLUMN 12003077659-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cuery Match 45.9%; Score 630.5; DB 8; Length 260;
RESULT 369
ID ADR72883 standard; protein; 260 AA.
PB Hunan ovarian cancer-related Fire-PD PD Hunan ovarian cancer-related Fire-PD PD Hunan ovarian cancer-related Fire-PD PD Hunan ovarian cancer-related Fire-PD PD Hunan ovarian cancer-related Fire-PD PD Hunan ovarian cancer-related Fire-PD PD Hunan ovarian cancer-related Fire-PD Hunan ovarian cancer-related Fire-PD PD Hunan ovarian cancer-related Fire-PD PD Hunan ovarian cancer-related Fire-PD PD Hunan ovarian cancer-related Fire-PD PD Hunan ovarian cancer-related Fire-PD PD Hunan ovarian cancer-related Fire-PD PD Hunan ovarian cancer-related Fire-PD PD Hunan ovarian cancer-related Fire-PD PD Hunan ovarian cancer-related Fire-PD PD Hunan ovarian cancer-related Fire-PD PD Hunan ovarian cancer-related Fire-PD PD Hunan ovarian cancer-related Fire-PD PD Hunan ovarian cancer-related Fire-PD PD Fire-PD PD Fire-PD PD Fire-PD PD Fire-PD PD Fire-PD PD Fire-PD PD Fire-PD PD Fire-PD PD Fire-PD PD Fire-PD PD Fire-PD PD Fire-PD PD Fire-PD PD Fire-PD PD Fire-PD PD Fire-PD PD Fire-PD PD Fire-PD PD Fire-PD PD Fire-PD PD Fire-PD PD Fire-PD PD Fire-PD Fire-PD PD Fire-PD PD Fire-PD PD Fire-PD PD Fire-PD PD Fire-PD PD Fire-PD PD Fire-PD PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD Fire-PD 
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Pred. No. 1.1e-40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 260;
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ry Match 45.9%; Score 630.5; DB 8; Length 260; t Local Similarity 50.2%; Pred. No. 1.1e-40;
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Human secreted protein encoded by gene 2 clone HWJAE49.
WO200055371-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 630.5; DB 8;
Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 50.9%; Score 627; DB 2; RESULT 371

ID AAB37985 standard; protein; 306 AA.

DE Human secreted protein encoded by care.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAX32853 standard; protein; 305 AA. Human serine protease protein sequence. JP11225765-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADNO4214 standard; protein; 260 AA. Antipsoriatic protein sequence #302.
WO2004028479-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 45.9%;
Local Similarity 50.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 50.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                            DIPIPPO V A.
BISEN A.
GANGOLLI E A.
RIEGER D K.
SPADERNA S K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-APR-2004.
(GETH ) GENENTECH INC.
                                                                                                                      MILLER C E.
RASTELLI L.
STONE D J.
PENA C E A.
SHENOY S G.
SHIMKETS R A.
ROTHENBERG M E
LEACH M D.
BERGHS C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-AUG-1999.
(SUNR ) SUNTORY LTD.
                                                            CATTERTON E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                               (DIPI/)
(EISE/)
(GANG/)
(RIEG/)
(SPAD/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                    (LEAC/)
(AGEE/)
(BERG/)
                                                                                                                                                                                                                    (PENA/)
(SHEN/)
(SHIM/)
(ROTH/)
(ANDE/)
                                                                                                                            (MILL/)
(RAST/)
(STON/)
                                                                                       (JIMM/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 370
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Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JR 378

MBBS719 standard; protein; 260 AA.

Mouse ischaemic condition related protein sequence SEQ ID NO:533.

WO2001881188-A2.
22-NOV-2001.

(UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.

A5 34: Score 622.5; DB 5; Length 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45.3%; Score 622.5; DB 2; Length 260; 49.0%; Pred. No. 4.5e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PD 24-SEP-1996.
PA (IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO KK.
Query Match
45.3%; Score 622.5; DB 2; Length 260;
Best Local Similarity 49.0%; Pred. No. 4.5e-40;
RESULT 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-DEC-1998.
(SMIK ) SMITHKLINE BEECHAM PLC.
Query Match
45.6%; Score 626.5; DB 2; Length 260;
CET * Annal Asimilarity 50.4%; Pred. No. 2.2e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZZ-JUL-1999.
(INCY-) INCYTE PHARM INC.
ery Match 45.3%; Score 622.5; DB 2; Length 260;
ery Match 49.8%; Pred. No. 4.5e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45.6%; Score 626.5; DB 3; Length 275; 50.4%; Pred. No. 2.3e-40;
                                                                                                                                                                                                                                                                                                                                                               Length 315;
                                                                                                           45.6%; Score 627; DB 3; Length 306; 50.9%; Pred. No. 2.4e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW10694 standard; protein; 260 AA.
Human recombinant neuropsin, used for antibody production
JP08245700-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45.3%; Score 622.5; DB 5;
49.0%; Pred. No. 4.5e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45.3%; Score 622.5; DB 5
49.0%; Pred. No. 4.5e-40;
                                                                                                                                                                                                           ABP41312 standard; protein; 315 AA.
Human ovarian antigen HCOQP78, SEQ ID NO:2464.
WO20200677-A1.
03-JAN-2002.
(HUMA-) HUMAN GENOME SCI INC.
45.64; Score 627; DB 5;
ery Match 45.64; Score 627; DB 5;
st Local Similarity 50.94; Pred. No. 2.4e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW87703 standard; protein; 260 AA.
A human serine protease designated HGBAB90.
EP887414-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADI17073 standard; protein; 260 AA.
Murine NOVX protein homologue SeqID 609.
WO200268649-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADI39731 standard; protein; 260 AA.
Mouse neuropsin protein.
USG642013-Bl.
USG42003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY06438 standard; protein; 260 AA.
Human protease HUPM-7.
WO9936550-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW12393 standard; protein; 260 AA.
Mouse neuropsin protein.
JP08311099-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB21311 standard; protein; 275 AA.
                                                        21-SEP-2000.
(HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MOUN ) MOUNT SINAI HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A...
1996.
207) SHIOZAKA S.
2-TY MATCh
Best Local Similarity 437
RESULT 377
ID AAY06438 standa-
DE Human prote-
PN WO9936F-
PA 22-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jalenic Control of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of the Month of
2000.

LY Match
Best Local Similarity 5.
RESULT 372
ID ABP41332 standar
DE Human ovarian PN W020020.
PD 03-7
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RESULT 380
ID AD139731 standard; pr
DE Mouse neuropsin prote
PN US6642013-B1.
PD 04-NOV-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
RESULT 375
ID AAW10694 standard; pr.
DE Human recombinant neu.
PN JP08245700-A.
PD 24-SEP-1996.
PA (IGAK-) IGAKU SEIBUTSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
RESULT 378
                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity RESULT 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human neuropsin.
WO200053776-A2.
14-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                          Best Loca
RESULT 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BERE
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vuery Match 45.0%; Score 618.5; DB 5; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PD 28-DEC-2000.

QUETH ) GENENTECH INC.

Query Match

45.0%; Score 618.5; DB 4; Length 250;

Best Local Similarity 48.2%; Pred. No. 8.7e-40;

RESULT 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45.0%; Score 618.5; DB 4; Length 250; 48.2%; Pred. No. 8.7e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
ery Match 45.0%; Score 618.5; DB 4; Length 250;
ery Match 48.2%; Pred. No. 8.7e-40;
                                                                                                                                                             Query Match
Best Local Similarity 49.0%; Pred. No. 4.5e-40;
RESULT 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 250;
                                                                                                                                                                                                                                                                                                                                                               Length 260;
                  Length 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY99390 standard; protein; 250 AA.
Human PRO1279 (UNQ649) amino acid sequence SEQ ID NO:170.
WOO20012708-A2.
09-MAR-2000.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB50479 standard; protein; 250 AA.
Human secreted protein encoded by gene 179 SEQ ID NO:427
WO200162891-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PD 14-SEP-2000.

PA (MOUN ) MOUNT SINAI HOSPITAL.

Query Match

Best Local Similarity 48.2%; Pred. No. 8.7e-40;

RESULT 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 45.0%; Score 618.5; DB 3; Best Local Similarity 48.2%; Pred. No. 8.7e-40; RESULT 385
(UYAR-) UNIV ARKANSAS MEDICAL SCI.

217 Match
45.3%; Score 622.5; DB 8;
51 Local Similarity 49.0%; Pred. No. 4.5e-40;
                                                                                                                                                                                                                                                                                                                                                               45.2%; Score 621.5; DB 5; 48.6%; Pred. No. 5.3e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jr 389
ABG61816 standard; protein; 250 AA.
Prostate cancer-associated protein #17.
                                                                                                                                                                                                                                                       AD117074 standard; protein; 260 AA.
Rat NOVX protein homologue SeqID 610.
W0200268649-AA.
(CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU83684 standard; protein; 250 AA.
Human PRO protein, Seq ID No 186.
WO200208288-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU12424 standard; protein; 250 AA.
Human PRO1279 polypeptide sequence.
WO200140466-A2.
(GFTH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 48.6%; Pred.
RESULT 383
ID AAB21325 standard; protein; 250 AA.
DE Human TLSP.
PN W0200053776-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB66139 standard; protein; 250 AA.
Protein of the invention #51.
WO200078961-A1.
                                                                                 ADI37155 standard; protein; 260 AA. Mouse neuropsin.
US2003199010-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200230268-A2.
18-APR-2002.
(EOSB-) EOS BIOTECHNOLOGY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-JAN-2002.
(GETH ) GENENTECH INC.
                                                                                                                                                         23-OCT-2003.
(UYAR-) UNIV ARKANSAS.
                    Query Match
Best Local Similarity
RESULT 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity RESULT 387
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RESULT 397
                                                            45.0%; Score 618.5; DB 5; Length 250; 48.2%; Pred. No. 8.7e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 618.5; DB 6; Length 250; Pred. No. 8.7e-40;
                                                                                                                                                                                                Score 618.5; DB 5; Length 250; Pred. No. 8.7e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45.0%; Score 618.5; DB 6; Length 250; 48.2%; Pred. No. 8.7e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45.0%; Score 618.5; DB 5; Length 250; 48.2%; Pred. No. 8.7e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 618.5; DB 6; Length 250;
Pred. No. 8.7e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45.0%; Score 618.5; DB 6; Length 250; 48.2%; Pred. No. 8.7e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 6; Length 250;
                                                                                                                                                                                                                                            ABB95526 standard; protein; 250 AA.
Human angiogenesis related protein PRO1279 SEQ ID NO: 208
WO200208284-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABO17868 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279
US20030312156-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AB031797 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003045687-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 618.5; DB 6
Pred. No. 8.7e-40;
                                                                                                          ABB84920 standard; protein; 250 AA.
Human PRO1279 protein sequence SEQ ID NO:208.
WO200200690-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lung cancer-associated polypeptide #332. WOS00286443-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABU81122 standard, protein, 250 AA. Human PRO polypeptide #253. US2003004311-AI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABU80831 standard; protein; 250 AA.
Human PRO polypeptide #93.
US2003036635-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (EOSB-) EOS BIOTECHNOLOGY INC
                                                                                                                                                                                            45.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 45.0%;
Local Similarity 48.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 45.0%;
Best Local Similarity 48.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 48.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                  GODOWSKI P J.
GURNEY A L.
HILLAN K J.
MARSTERS S A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (PANJ) PAN J.
(PAON) PAONI N F.
(STED) STEBHAN J F.
(WILL) WILLIAMS P M.
(WOOD) WOOD W I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-FEB-2003.
(GETH ) GENENTECH INC.
Lary Match
Best Local Similarity
RESULT 390
ID ABB64920 stand<sup>2</sup>
DE Human PROJ<sup>2</sup>
PN WO2002<sup>2</sup>
PD 03<sup>2</sup>
                                                                                                                                                            03-JAN-2002.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                   GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                   GERBER H.
GERRITSEN M E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-MAR-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-JAN-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity RESULT 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                BAKER K P.
FERRARA N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                     GODDARD A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-FEB-2003
                                                                                                                                                                                            Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                (BAKE/)
(FERR/)
(GERB/)
(GODD/)
(GODO/)
(GURN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 394
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Query Match 45.0%; Score 618.5; DB 6; Length 250; Best Local Similarity 48.2%; Pred. No. 8.7e-40; RESULT 403
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                                                                                           Length 250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 618.5; DB 6; Length 250; Pred. No. 8.7e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 618.5; DB 6; Length 250; Pred. No. 8.7e-40;
                                                                                                                                                                                                                                                    Length 250;
                                                                                                                                                                                                                                                                                                                                                                                                          Length 250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 6; Length 250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABU82140 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003088063-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADA46025 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279
US2003022328-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABU67098 standard; protein; 250 AA.
Human secreted/transmembrane, PRO, protein SEQ ID
US2003032155-A1.
                                                                                                                                                                                                                                      Query Match 45.0%; Score 618.5; DB 6;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 399
                                                                                                                                                                                                                                                                                                                                                                                                        45.0%; Score 618.5; DB 6; 48.2%; Pred. No. 8.7e-40;
                                                                                               Score 618.5; DB 6;
Pred. No. 8.7e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 618.5; DB 6;
Pred. No. 8.7e-40;
                                                                                                                                                 ABU59903 standard; protein; 250 AA.
Novel secreted and transmembrane protein PRO1279
US2003017563-A1.
                                                                                                                                                                                                                                                                                                       ABO25093 standard; protein; 250 AA.
Human secreted/transmembrane protein (PRO) #253.
US20036179-A1.
20-FEB-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 45.0%; Score 618.5; DB 6 Best Local Similarity 48.2%; Pred. No. 8.7e-40; RESULT 401
ABU66822 standard, protein, 250 AA.
Human PRO polypeptide #253.
US2003036180-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human PRO polypeptide #253.
US2003054517-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADA76456 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003073212-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABJ72320 standard; protein; 250 AA
                                        USZUCZZ
20-FBE-2003.
(GETH ) GENENTECH INC.
MATCh '-'larity 48.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 45.0%;
Best Local Similarity 48.2%;
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Best Local Similarity 48.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-APR-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                            23-JAN-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-JAN-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human PRO1279 protein.
US2003050448-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-MAR-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-MAR-2003.
(GETH ) GENENTECH INC.
                                                                                             Query Match
Best Local Similarity
RESULT 398
                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity RESULT 400
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Best Local Similarity
RESULT 406
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Best Local Similarity
RESULT 405
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Human PRO polypeptide #253.
US2003068794-A1.
                                 10-APR-2003
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Pred. No. 8.7e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 618.5; DB 6; Length 250; Pred. No. 8.7e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45.0%; Score 618.5; DB 6; Length 250; 48.2%; Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
                                                                                 DB 6; Length 250;
                                                                                                                                                                                                                Score 618.5; DB 6; Length 250;
Pred. No. 8.7e-40;
                                                                                                                                                                                                                                                                                                                                               DB 6; Length 250;
                                                                                                                                                                                                                                                                                                                                                                                             ADA86534 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003082711-A1.
                                                                                                                                ADB19514 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003068796-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AB033632 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PR01279
US2003073130-A1.
                                                                                   Score 618.5; DB 6
Pred. No. 8.7e-40;
                                                                                                                                                                                                                                                                                                                                               Score 618.5; DB 6
Pred. No. 8.7e-40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADBI6098 standard; protein; 250 AA. Human PRO polypeptide #253. US2003087350-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADA47884 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003073215-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABO44736 standard; protein; 250 AA. Novel human secreted protein #179. US2003065160-A1.
                                                                                                                                                                                                                                              JT 408
ADB28055 standard; protein; 250 AA. Human PRO polypeptide #253.
US2003082704-A1.
01-MAY-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADB30686 standard; protein; 250 AA
   ADA61729 standard; protein; 250 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     250 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45.0%;
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(HUMA-) HUMAN GENOME SCI INC.
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RESULT 415
                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 48.2%;
RESULT 409
                                                                                                                                                                                                           Best Local Similarity 48.2%;
RESULT 408
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Human PRO polypeptide #253.
US2003068795-A1.
                                                                                                  48.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 48.2%;
                                                                                   45.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-MAY-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
Query Match 4
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(GETH ) GENENTECH INC.
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                                                                                                                                                                                10-APR-2003.
(GETH ) GENENTECH INC
                                                  13-MAR-2003.
(GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity RESULT 411
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Best Local Similarity
RESULT 413
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                                                                                                Best Local Similarity
RESULT 407
                    Homo sapiens.
US2003049816-A1.
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Length 250;
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              Length 250;
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Novel human secreted and transmembrane protein PRO1279.
US2003073211-A1.
                                                                    ADA85982 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003082693-A1.
01-MAY-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADABT637 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003087345-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADA91931 standard, protein, 250 AA.
Novel human secreted and transmembrane protein PRO1279
US2003082694-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 45.0%; Score 618.5; DB 6; Len Best Local Similarity 48.2%; Pred. No. 8.7e-40; RESULT 423

ID ADB18955 standard; protein; 250 AA.

DE Novel human secreted and trant PD US-2003073211-A1.

PD 17-APR-2007
                                                                                                                                                                                                                                                                                               Query Match 45.0%; Score 618.5; DB 6;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 618.5; DB 6;
Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
                DB 6;
                                                                                                                                                          45.0%; Score 618.5; DB 6; 48.2%; Pred. No. 8.7e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 6;
                Score 618.5; DB 6,
Pred. No. 8.7e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 618.5; DB 6
Pred. No. 8.7e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A ADB16839 standard; protein; 250 AA.

Human PRO polypeptide #253.

VG2003087349-A1.

OG-MAY-2003.

OG-MAY-2003.

Query Match
                                                                                                                                                                                                                                                                                                                                                      ADA79498 standard, protein, 250 AA.
Human PRO polypeptide #253.
US2003082763-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADA94170 standard, protein; 250 AA.
Human PRO polypeptide #253.
                                                                                                                                                                                                              250 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45.0%;
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                45.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 48.2%;
RESULT 419
                                                                                                                                                                                                          DA97194 standard; protein;
Human PRO polypeptide #253.
US20030082705-A1.
O1-MAY-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
GENENTECH INC
                  Query Match
Best Local Similarity
RESULT 416
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RESULT 421
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Best Local Similarity
RESULT 422
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RESULT 424
ID ADA94170 standard,
DE Human PRO polvnent'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
RESULT 420
                                                                                                                                                              Query Match
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Chery Match 45.0%;
Best Local Similarity 48.2%;
RESULT 434
                                                                                                                                                                                                                                                        01-MAY-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                                               17-APR-2003.
(GETH ) GENENTECH INC.
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RESULT 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity RESULT 441
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Best Local Similarity
RESULT 442
 01-MAY-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 437
1D ADA4712
DE Human F
PN US2003C
PD 17-APR-
                                                                                                                                                                                                                                                                                                                                                                                                                      vuery Match
45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 45.0%; Score 618.5; DB 6; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 618.5; DB 6; Length 250; Pred. No. 8.7e-40;
                                             45.0%; Score 618.5; DB 6; Length 250; 48.2%; Pred. No. 8.7e-40;
                                                                                                                                                                           Score 618.5; DB 6; Length 250;
Pred. No. 8.7e-40;
                                                                                                                                                                                                                                                                                                         6; Length 250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 618.5; DB 6; Length 250;
Pred. No. 8.7e-40;
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                                                                           Aubrunb6 standard; protein; 250 AA.

Novel human secreted and transmembrane protein PRO1279.
US2003082691-A1.
01-MAY-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                           Novel human secreted and transmembrane protein PRO1279, US2001044945-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADVOL human secreted and transmembrane protein PRO1279.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADA84878 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003082708-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 6;
                                                                                                                                                                                                                                                                                                         Score 618.5; DB 6
Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADB24865 standard; protein; 250 AA.
Human PRO polypeptide SEQ ID NO 506.
US20030777713-A1.
                                                                                                                                                                                                                       ADB13378 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003082710-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADA74632 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003068798-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADA82389 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003082701-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADA75352 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003073216-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45.0%;
                                                                                                                                                                         Query Match 45.0%;
Best Local Similarity 48.2%;
RESULT 426
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                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 48.2%;
RESULT 427
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Best Local Similarity 48.2%;
RESULT 431
               24-APR-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                       06-MAR-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
Query Match 4
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(GETH ) GENENTECH INC
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(GETH ) GENENTECH INC.
                                                         Best Local Similarity
RESULT 425
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US2003077722-A1.
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Best Local S
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vuery Match 45.0%; Score 618.5; DB 6; Length 250; Best Local Similarity 48.2%; Pred. No. 8.7e-40; RESULT 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 45.0%; Score 618.5; DB 6; Length 250; Best Local Similarity 48.2%; Pred. No. 8.7e-40; RESULT 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 618.5; DB 6; Length 250; Pred. No. 8.7e-40;
Score 618.5; DB 6; Length 250;
Pred. No. 8.7e-40;
                                                                                                                                                         Length 250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45.0%; Score 618.5; DB 6; Length 250; 48.2%; Pred. No. 8.7e-40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GETH ) GENENTECH INC. (GETH ) GENENTECH INC. 45.0%; Score 618.5; DB 6; ery Match 48.2%; Pred. No. 8.7e-40;
                                                                                                                                                       Score 618.5; DB 6;
Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADB25425 standard; protein; 250 AA. Human PRO polypeptide SEQ ID NO 506. US2003077715-A1.
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24-app.
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                                                   ADB30134 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003073214-A1.
                                                                                                                                                                                            RESULT 435
ID AAA80662 standard; protein; 250 AA.
DE Human PRO polypeptide #253.
PN US2003082761-A1.
                                                                                                                                                                                                                                                                                                                                                                       ADA75904 standard; protein; 250 AA. Human PRO polypeptide #253. US2003082703-A1. COL-MAY-2003 (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADA47129 standard, protein, 250 AA.
Human PRO polypeptide #253.
US2003073210-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADB26951 standard; protein; 250 AA. Human PRO polypeptide #253. US2003092147-A1. 15-MAY-2003. (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADB31238 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003096386-A1.
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Best Local Similarity 48.2%;
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Human PRO polypeptide #253. US20032699-A1.
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Human PRO polypeptide #253.
US2003059909-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADB29159 standard; protein; 250 AA. Human PRO polypeptide #253. US2003082706-A1.
                                             ADB18403 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003077710-A1.
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   45.0%;
                                                                                                                                      Query Match
Best Local Similarity 48.2%;
RESULT 453
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                          24-APR-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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RESULT 458
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RESULT 454
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RESULT 455
Query Match
Best Local Similarity
RESULT 452
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Best Local Similarity 48.2%; Score 618.5; DB 6; Length 250;
RESULT 45.1

ID MAT7663 standard; protein; 250 AA.

BE Human PRO polypeptide #253.

PD 10-APR-2003

PD 6ETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Length 250;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 45.0%; Score 618.5; DB 6; Length 250; Best Local Similarity 48.2%; Pred. No. 8.7e-40; RESULT 446
                                                                                                                                                               45.0%; Score 618.5; DB 6; Length 250; 48.2%; Pred. No. 8.7e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 6; Length 250;
                       45.0%; Score 618.5; DB 6; Length 250; 48.2%; Pred. No. 8.7e-40;
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                                                                                                                                                                                                                                                                                                     Length 250;
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Novel human secreted and transmembrane protein PRO1279.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABO34343 standard; protein; 250 AA.
Human secreted/transmembrane polypeptide PRO 1279.
US2003044934-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 6;
                                                                                                                                                                                                                                                                                                       DB 6;
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Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 448
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Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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                                                                                                                                                                                                            ADB24313 standard; protein; 250 AA. Human PRO polypeptide SEQ ID NO 506. US2003077714-A1. 24-APR-2003. CA-APR-2003.
                                                                                                                                                                                                                                                                                                                                                          ADA96642 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003082690-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADAB1214 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003082702-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADA96090 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003082759-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADB26399 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003082760-A1.
                                                                               ADA61166 standard; protein; 250 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 48.2%;
RESULT 449
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Best Local Similarity 48.2%;
RESULT 450
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Best Local Similarity 48.2%;
RESULT 445
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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2.003.
2.14) GENENTECH I.
2.17 MATCh
B881 Local Similarity 47
ID ADA96090 stand*
DB Human PRO T
PN US2003^C
PN US2003^C
PN PS
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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            PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 4
RESULT 443
                                                                                                                                      13-MAR-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                   Query Match
Best Local Similarity
RESULT 444
ID ADB24313 standard; p
                                                                                                   Homo sapiens.
US2003049817-A1.
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45.0%; Score 618.5; DB 7; Length 250;
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Pred. No. 8.7e-40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 250;
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Score 618.5; DB 7; Length 250; Pred. No. 8.7e-40;
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                                                                                                                                                                  Length 250;
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Novel human secreted and transmembrane protein PRO1279.
US2003054516-A1.
20-MAR-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                 ADA87086 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003082709-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADA88189 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279
US2003082700-A1.
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12. Match
45.0%; Score 618.5; DB 7;

14. Local Similarity 48.2%; Pred. No. 8.7e-40;
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Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 456
                                                                                                                                                                                                                                                                                                                                   DB 7;
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Pred. No. 8.7e-40;
                                                                                                                                                                  Score 618.5; DB 7;
Pred. No. 8.7e-40;
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Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 48.0%; Score 618.5; DB 7 Best Local Similarity 48.2%; Pred. No. 8.7e-40; RESULT 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45.0%; Score 618.5; DB 7 48.2%; Pred. No. 8.7e-40;
                                                                                                                                                                                                                                                                                                                                                                                                ABO44485 standard; protein; 250 AA.
Human secreted/transmembrane protein PRO1279.
US2003044841-A1.
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Novel human secreted and transmembrane protein PRO1279
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(GETH ) GEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABJ72150 standard; protein; 250 AA.
Human membrane bound receptor/protein PRO1279 amino acid sequence.
US2003065147-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 618.5; DB 7; Length 250; Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
                                                                                                                                                                                         45.0%; Score 618.5; DB 7; Length 250; 48.2%; Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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                                                                                                          ABO33509 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003073129-A1.
                                                                                                                                                                                                                                         ADA88741 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279
US2003073213-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADB22436 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279
US2003087344-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 7;
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Pred. No. 8.7e-40;
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                                                                           48.2%; Pred. No. 8.7e-40;
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                                                                                                                                                                                                                                                                                                                                                                        ADA97746 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003082686-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADB27503 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003022239-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADA67127 standard; protein; 250 AA. Human PRO polypeptide #253.
US2003068793-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADB22988 standard; protein; 250 AA. Human PRO polypeptide #253. US2003077711-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADA92483 standard; protein; 250 AA
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Best Local Similarity 48.2%;
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RESULT 470
Best Local Similarity 4.
RESULT 461
ID AB033509 standar
DE Novel humar
PN US20030***
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                                                                          17-APR-2003.
(GETH ) GENENTECH INC
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(GETH ) GENENTECH INC.
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                                                                                                                                                                                                     Best Local Similarity RESULT 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-MAY-2003.
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                                                                                                                                                                                            Query Match
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Length 250;
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                                                                                                                                                                                                                            Novel human secreted and transmembrane protein PRO1279.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADB73123 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003096968-A1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADB38798 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003082766-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUDOO /18 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
                                                                                                                                                                                                                                                                                                                                                                                ADB80782 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADB78405 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279
US2003092889-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADB38246 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279
US2003087347-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            uuery Match
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 474
                                                  Score 618.5; DB 7;
Pred. No. 8.7e-40;
                                                                                                                                                                                                                                                                                                                           Score 618.5; DB 7;
Pred. No. 8.7e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45.0%; Score 618.5; DB 7; 48.2%; Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 618.5; DB 7;
Pred. No. 8.7e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 618.5; DB 7;
Pred. No. 8.7e-40;
                                                                                                                                                                                         Score 618.5; DB 7
Pred. No. 8.7e-40;
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                                                                                                 ADBI5546 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003087352-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADB85053 standard; protein; 250 AA. Human PRO polypeptide #93.
                                                                                                                                                                                                                                                                         US20030,...
17-APR-2003.
(GETH ) GENENTECH INC.
45.0%; St
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                                                45.0%;
                                                                                                                                                                                    Query Match
Best Local Similarity 48.2%;
RESULT 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45.0%;
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US2003082712-A1.
01-MAY-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 476
                                                Query Match
Best Local Similarity
RESULT 471
                                                                                                                                                                                                                                                                                                                                          Best Local Similarity RESULT 473
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Best Local Similarity
RESULT 477
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RESULT 475
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10-APR-2003.
(GETH ) GENENTECH INC.
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(GETH ) GEN
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                                       Query Match
                                                                                                                                                                                          Query Match
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                                                    Score 618.5; DB 7; Length 250;
Pred. No. 8.7e-40;
                                                                                                                                                                                                                                                                                                                                                              Length 250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45.0%; Score 618.5; DB 7; Length 250; 48.2%; Pred. No. 8.7e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 45.0%; Score 618.5; DB 7; Length 250; Best Local Similarity 48.2%; Pred. No. 8.7e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45.0%; Score 618.5; DB 7; Length 250; 48.2%; Pred. No. 8.7e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45.0%; Score 618.5; DB 7; Length 250; 48.2%; Pred. No. 8.7e-40;
                                                                                                                                                                                                             7; Length 250;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUD/BLD9 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US200392886-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADB83922 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003069397-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADB39631 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003082764-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADB47254 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003082687-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 618.5; DB 7,
Pred. No. 8.7e-40;
                                                                                                                                                                                                                                                                                                                                                              45.0%; Score 618.5; DB 7 48.2%; Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
                                                                                                                                                                                                           Score 618.5; DB 7
Pred. No. 8.7e-40;
                                                                                                                                                                                                                                                                                                                                                                                                     Ovarian cancer-associated protein #81. 27-psc-act. 27-psc-act. 27-psc-act.
                                                                                                                 ADB89798 standard; protein; 250 AA.
                                                                                                                                                                                                                                                                ADB90530 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003082762-AI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADB87225 standard; protein; 250 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADB84807 standard; protein; 250 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-DEC-2002.
(EOSB-) EOS BIOTECHNOLOGY INC.
                                                        45.0%;
                                                                                                                                                                                                           45.0%;
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Best Local Similarity 48.2%;
RESULT 485
                                                                                                                                   Human PRO polypeptide #253.
US2003082698-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human PRO polypeptide #93.
US2003092890-A1.
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US2003088067-A1.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC
                                       (GETH ) GENENTECH INC.
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Best Local Similarity
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                                                                      Best Local Similarity RESULT 480
 US2003073817-A1.
                       17-APR-2003
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                                                                                                                                                                                                                                                RESULT 481
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24.APR-2003.
(GETH ) GENENTECH INC.
(ery Match 45.0%; Score 618.5; DB 7; Length 250;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 250;
Length 250;
                                                                                                                                                                                    ADB73077 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003092887-A1.
                                                                                                                                                                                                                                                                                                                      ADB77466 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003082696-A1.
01-MAY-2003.
(GETH ) GENENTECH INC.
7;
                                                                                                                                                                                                                                                                                                                                                                                                         45.0%; Score 618.5; DB 7; 48.2%; Pred. No. 8.7e-40;
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                                                                                                                                                                                                                                                                      DB 7;
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Score 618.5; DB 7
Pred. No. 8.7e-40;
                                                                                                                                  Score 618.5; DB 7
Pred. No. 8.7e-40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADB34623 standard; protein; 250 AA. Human PRO polypeptide SEQ ID NO 506. US2003077777-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human PRO polypeptide SEQ ID NO 506. 182003077719-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADB36279 standard; protein; 250 AA. Human PRO polypeptide SEQ ID NO 506. US2003077720-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein; 250 AA.
                                                 protein; 250 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prostate cancer marker protein. W02003009814-A2. (HEB-2003. (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                  45.0%;
                                                                                                                                                                                                                                                                 Best Local Similarity 48.2%;
RESULT 491
45.0%;
               48.28;
                                                                 Human PRO polypeptide #253
US2003082697-A1.
01-MAY-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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        Best Local Similarity RESULT 489
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RESULT 496
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Best Local Similarity
RESULT 493
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Best Local Similarity
RESULT 494
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Best Local Similarity
RESULT 497
                                                                                                                                                Best Local Similarity RESULT 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADB75388 standard;
                                                 ADB86861 standard;
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RESULT 498

Best Loca RESULT 499

Best RESULT

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45.0%; Score 618.5; DB 7; Length 250;
   Score 618.5; DB 7; Length 250;
Pred. No. 8.7e-40;
                                                                                                                                                                                                                                                                               Length 250;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADC5/434 Standard; protein; 250 AA.
Novel human secreted and transmembrane protein Seg ID506.
US2003081366-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADC53686 standard, protein; 250 AA.
Novel human secreted and transmembrane protein Seg ID506.
US2003087364-A1.
                                                                                                                                                                                                                                                                                                                               ADC53080 standard; protein; 250 AA.
Novel human secreted and transmembrane protein Seg ID506
US2003087365-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADCS4725 standard; protein; 250 AA. Novel human secreted and transmembrane protein Seg ID506
                                                                                                                                                                            AUC47513 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003088072-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADCOG625 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003087367-A1.
                                                    ADC49652 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003088071-A1.
08-MAY-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADC51100 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003087361-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 618.5; DB 7;
Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
                                                                                                                                        Score 618.5; DB 7;
Pred. No. 8.7e-40;
                                                                                                                                                                                                                                                                               Score 618.5; DB 7;
Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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08-003087362-A1.
   45.0%;
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RESULT 511
                                                                                                                                        45.0%;
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Best Local Similarity 48.2%;
RESULT 509
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RESULT 512
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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                 Best Local Similarity RESULT 507
                                                                                                                                                      Best Local Similarity RESULT 508
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RESULT 513
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(GETH ) GEN
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(GETH ) GEN
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   Query Match
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                                                                                                                                                        Score 618.5; DB 7; Length 250; Pred. No. 8.7e-40;
                                                                                                                                                                                                                                                                                               Length 250;
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Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
                   45.0%; Score 618.5; DB 7; Length 250; 48.2%; Pred. No. 8.7e-40;
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                                                                    ADB46674 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279
US2003082692-A1.
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Novel human secreted and transmembrane protein PRO1279.
US2003088064-A1.
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Novel human secreted and transmembrane protein PRO1279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADC49135 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279
US2003088070-A1.
08-MAY-2003.
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Pred. No. 8.7e-40;
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                                                                                                                                                                                                                                                                                               Score 618.5; DB 7
Pred. No. 8.7e-40;
                                                                                                                                                                                                         ADC18039 standard; protein; 250 AA.
Human PRO polypeptide #51.
US2003064925-A1.
                                                                                                                                                                                                                                                                                                                                       Human PRO polypeptide #93.
US2003088065-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADC21905 standard; protein; 250 AA
Human PRO polypeptide #93.
US2003096969-A1.
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Local Similarity 48.2%;
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Best Local Similarity 48.2%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Query Match
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RESULT 504
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Best Local Si
RESULT 506
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ADC78133 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003096972-A1.
RESULT
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Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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                                                                                                                                                    AUCS6087 standard; protein; 250 AA.
Novel human secreted and transmembrane protein Seq ID506.
US2003087360-A1.
                                                                                                                                                                                                                                                                                                    ADCS8657 standard; protein; 250 AA.
Novel human secreted and transmembrane protein Seg ID506.
US2003087346-A1.
                             ADC55209 standard; protein; 250 AA.
Novel human secreted and transmembrane protein Seg ID506.
US2003087359-A1.
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Novel human secreted and transmembrane protein PRO1279.
US2003105288-AI.
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Novel human secreted and transmembrane protein PRO1279
US2003087348-A1.
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Novel human secreted and transmembrane protein PRO1279
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                                                                                                                   Score 618.5; DB 7;
Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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   48.2%; Pred. No. 8.7e-40;
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Human PRO polypeptide #253.
US2003194773-A1.
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Human PRO polypeptide #253.
US2003194770-A1.
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RESULT 523
                                                                                                                    45.0%;
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Best Local Similarity 48.2%;
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Human PRO polypeptide #253.
US2003194776-A1.
                                                                                                                                                                                                                                                   Match 45.0%;
Local Similarity 48.2%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 524
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Best Local Similarity
     Best Local Similarity
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                    RESULT
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Score 618.5; DB 7; Length 250;
Pred. No. 8.7e-40;
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Novel human secreted and transmembrane protein PRO1279.
US2003087358-A1.
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Novel human secreted and transmembrane protein PRO1279.
US2003088066-A1.
8-MAY-2003.
                                                                                                           Novel human secreted and transmembrane protein PRO1279. US2003087354-A1.
                                                                                                                                                                                                                                 ADD06368 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003073816-A1.
                                                                                                                                                                                                                                                                                                                                                                    ADC80691 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279
US2003092103-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADD10497 standard; protein; 250 AA.
ADD10497 standard; protein; 250 AA.
Human secreted/transmembrane PRO polypeptide #104
US2003105011-A1.
05-JUN-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                  45.0%; Score 618.5; DB 7;
48.2%; Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
                                           Score 618.5; DB 7;
Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 532
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08-MAY-2003.

(GFH ) GENENTECH INC.

45.0%; Score 618.5; DB 7;

(ery Match

45.2%; Pred. No. 8.7e-40;
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Human PRO polypeptide #253.
US2003194771-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADD11198 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003194774-A1.
                                                                                                  ADD04735 standard; protein; 250 AA
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45.0%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 527
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Best Local Similarity
RESULT 531
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RESULT 526
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Novel human secreted and transmembrane protein PRO1279.
US20034377A1.
30-CCT-2003
(GETH ) GENENTECH INC.
                                                                               Query Match
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                                                                                             Query Match
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
                                                                                                                                                                                                                                                                                                    ADD50850 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003105291.A1.
05-JUN-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADD41321 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003203438-A1.
30-OCT-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Beet Local Similarity 48.2%; Pred. No. 8.7e-40; RESULT AD51096 standard; protein; 250 AA.

DE Novel human secreted and transmembrane protein PRO1279.

PN US2003105290-A1.
ADD11457 standard; protein; 250 AA.
Human secreted/transmembrane PRO polypeptide #104.
US2003105013-A1.
05-JUN-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45.0%; Score 618.5; DB 7 48.2%; Pred. No. 8.7e-40;
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ID ADD70685 standard; protein; 250 AA.
DE Human secreted/transmembrane protein PRO1279.
PN US2003099625-A1.
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Human secreted/transmembrane protein PRO1279.
US2003083462-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADD52460 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003194769-A1.
                                                                                                                                                   ADD09608 standard, protein, 250 AA.
Human PRO polypeptide #253.
US2003194775-Al.
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US2003194792-A1.
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                                                                                                                                                                                                                                                 45.0%;
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RESULT 541
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Local Similarity 48.2%;
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Best Local Similarity 48.2%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC
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(GETH ) GENENTECH INC.
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ID ADD70208 standard; protein; 250 AA.

DE Human secreted/transmembrane protein PRO1279.

BN US2003054406-A1.

PD 20-MAR-2003.

PA (GETH) GENENTECH INC.

Query Match 45.0%; Score 618.5; DB 7; Length 250;

Best Local Similarity 48.2%; Pred. No. 8.7e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 45.0%; Score 618.5; DB 7; Length 250; Best Local Similarity 48.2%; Pred. No. 8.7e-40; RESULT 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 618.5; DB 7; Length 250; Pred. No. 8.7e-40;
  Length 250;
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(GETH ) GENENTECH INC.
(ery Match 45.0%; Score 618.5; DB 7; Length 250;
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Novel human secreted and transmembrane protein PRO1279.
                                                                                                                                                                                                        ADD37250 standard; protein; 250 AA.
Human secreted/transmembrane PRO polypeptide #104.
US2003105012-A1.
                                                                                                                                                                                                                                                                                                      Score 618.5; DB 7;
Pred. No. 8.7e-40;
Score 618.5; DB 7;
Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
                                                                                                                                                                                                                                                                                                                                                         ADD38329 standard; protein; 250 AA.
Human secreted/transmembrane protein PRO1279.
US2003096955-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADD39285 standard; protein; 250 AA.
Human secreted/transmembrane protein PRO1279.
US2003096954-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADD51908 standard; protein; 250 AA. Human PRO polypeptide #253. US200319479-A1. 16-OCT-2003. (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADD02707 standard; protein; 250 AA. Human PRO polypeptide #253. US2003203431-A1. 30-OCT-2003. (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          250 AA.
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45.0%;
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RESULT 546
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Best Local Similarity 48.2%;
RESULT 549
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FESULT 550
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RESULT 551
ID ADD02141 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADD02141 standard; protein;
Human PRO polypeptide #253.
1052003203430-Al.
30-CCT-2003.
(GETH.) GENENTECH INC.
                                                                                                                                                                                                                                                                    05-JUN-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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              Best Local Similarity
RESULT 544
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15-MAY-2003. (GETH ) GENENTECH INC.
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Pred. No. 8.7e-40;
                                                    45.0%; Score 618.5; DB 7; Length 250; 48.2%; Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
                                                                                                                                                                                          Score 618.5; DB 7
Pred. No. 8.7e-40;
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Human secreted/transmembrane protein PRO1279.
US2003069179-A1.
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ADE20072 standard; protein; 250 ÅA.
Man secreted/transmembrane protein PRO1279.
US2003092883-A1.
                                                                                                                                                                                                                                           ADD38808 standard; protein; 250 AA.
Human secreted/transmembrane protein PRO1279.
US2003092061-A1.
                                                                                                                                                                                                                                                                                                                                                                                 ADD40239 standard; protein; 250 AA.
Human secreted/transmembrane protein PRO1279.
US2003082627-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADD91536 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003199055-A1.
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Human PRO polypeptide #253.
US2003199057-A1.
                                                                                                        ADD50331 standard; protein; 250 AA.
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Human PRO polypeptide #253.
US2003199030-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADD51342 standard; protein; 250 AA
                                                                                                                                                                                          45.0%;
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RESULT 555
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Local Similarity 48.2%;
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Best Local Similarity 48.2%;
                                                                       48.28;
                                                                                                                        Human PRO polypeptide #93.
US2003096970-Al.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                   (GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 558
                                                                                                                                                                                          Query Match
Best Local Similarity
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                                                                Best Local Similarity
RESULT 553
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   US2003203432-A1.
                                                                                                                                                            22-MAY-2003
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Best Locc.
RESULT 559
ID ADD91'
DE Humr
PN US'
PD ?
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ID ADD388
DE Human
PN US2003
PD 15-MAY
PA (GETH
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Query Match 45.0%; Score 618.5; DB 7; Length 250; Best Local Similarity 48.2%; Pred. No. 8.7e-40; RESULT 562
ID ADE32447 standard; protein; 250 AA.
DE Novel human secreted and transmembrane protein PR01279.
PN US2001194765-A1.
PD 16-OCT-2003.
PD 16-OCT-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45.0%; Score 618.5; DB 7; Length 250; 48.2%; Pred. No. 8.7e-40;
                                                                                                                                                                                                                                                                                                                    Length 250;
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A ADE31551 standard; protein; 250 AA.

DB Novel human secreted and transmembrane protein PRO1279.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADE34103 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279
US2003194791-A1.
                                                                                                                                                                Score 618.5; DB 7;
Pred. No. 8.7e-40;
                                                                                                                                                                                                                                                                                                                    Score 618.5; DB 7;
Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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23-OCT-2003.
(GTT) GENENTECH INC.
(GTT) SCORE 618.5; DB 7;
lery Match
A5.0%; Score 618.5; DB 7;
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Pred. No. 8.7e-40;
                                                                                                                                                                                                                       ADE22379 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003199056-A1.
                                                                                                                                                                                                                                                                                                                                                                        ADD79603 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003203428-AI.
30-OCT-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LT 565
AD842139 standard; protein; 250 AA.
AD842139 Standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003194772-A1.
16-OCT-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADE17956 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003199023-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADD92088 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003199053-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADD80155 standard; protein; 250 AA. Human PRO polypeptide #253. US2003207417-A1. 06-NOV-2003.
                                                                                                                                                                45.0%;
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                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 48.2%;
RESULT 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48.2%;
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(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                 23-OCT-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 566
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Best Local Similarity
RESULT 567
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RESULT 569
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                                                                                                                                                                              Best Local Similarity RESULT 563
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30-0CT-2003.
(GETH ) GENENTECH INC.
45.0%; Score 618.5; DB 7; Length 250;
Score 618.5; DB 7; Length 250; Pred. No. 8.7e-40;
                                                                                                                                                                                                                                                                    DB 7; Length 250;
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                                              ADE32999 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003194766-A1.
16-OCT-2003.
(GETH ) GENENTECH INC.
                                                                                                                                  Score 618.5; DB 7;
Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
                                                                                                                                                                                                                                                                  45.0%; Score 618.5; DB 7, 48.2%; Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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Human secreted/transmembrane protein PRO1279.
US2003204053-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADF55859 standard; protein; 250 AA.
Human secreted/transmembrane protein PRO1279.
US2003204054-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human PRO polypeptide #253.
032003199034-A1.
                                                                                                                                                                               ADE42691 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003199032-A1.
23-OCT-2003.
                                                                                                                                                                                                                                                                                                                ADD80707 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003207418-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                ADD89735 standard; protein; 250 AA. Human PRO polypeptide #253. US2003199058-A1. C3-OCT-2003 (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADE92947 standard; protein; 250 AA. Human PRO polypeptide #253.
US2003194777-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 48.2%;
RESULT 585
 45.0%;
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                                                                                                                                 45.0%;
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Best Local Similarity 48.2%;
RESULT 584
ID ADE41019 standard; protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADB41019 standard; protein;
Human PRO polypeptide #253.
US2003199031-A1.
23-OCT-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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RESULT 582
             Best Local Similarity
RESULT 580
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RESULT 583
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Best Local Similarity
RESULT 587
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RESULT 586
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                                                                                                                                  Query Match
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                                                                                                                                                  DB 7; Length 250;
                                                                                                                                                                                                                                                                                 Length 250;
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Pred. No. 8.7e-40;
                 45.0%; Score 618.5; DB 7; Length 250; 48.2%; Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
                                                                                                                                                                                                                                                                                 DB 7;
                                                                                                                                                  Score 618.5; DB 7
Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
                                                               ADE49983 standard; protein; 250 AA.
Human secreted/transmembrane protein PRO1279.
US2003082626-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADE21541 standard; protein; 250 AA.
Human secreted/transmembrane protein PRO1279.
US2003082628-A1.
                                                                                                                                                                                           ADD93192 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003194768-A1.
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US2003203429-A1.
                                                                                                                                                                                                                                                                                                                              ADE19612 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003199025-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADE43256 standard; protein; 250 AA. Human PRO polypeptide #253.
US2003199033-A1.
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Best Local Similarity 48.2%;
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RESULT 578

ID ADES2931 standard; protein,
DE Human PRO polypeptide #253.
PN US2003199064-A1.
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Human PRO polypeptide #253.
US2003199059-Al.
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Human PRO polypeptide #253.
US2003199026-A1.
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PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 48.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
(GETH ) GENENTECH INC
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(GETH ) GENENTECH INC.
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                    Best Local Similarity
RESULT 571
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                 Query Match
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Score 618.5; DB 7; Length 250; Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
                                                                                                                             Score 618.5; DB 7; Length 250;
Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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Novel human secreted and transmembrane protein PRO1279.
US2003207385-A1.
                                                                                                                                                                  AUG21227 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADH55988 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003207379-A1.
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Novel human secreted and transmembrane protein PRO1279
US2003207381-A1.
                                   ADG21656 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279
US2003207355-AI.
                                                                                                                                                                                                                                                                       Score 618.5; DB 7;
Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
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Human secreted/transmembrane protein PRO1279.
US2003065142-A1.
                                                                                                                                                                                                                                                                                                                       MDF97632 standard; protein; 250 AA. Human PRO Polypeptide #253. US2003207370-A1. O6-NCV-2003. (GFTH) GENENTECH INC. 45.0%; Score 61 yeary Match similarity 48.2%; Pred. Nc 808t Local Similarity 48.2%; Pred. Nc
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Human PRO polypeptide #253.
US2003207372-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein; 250 AA
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03-APR-2003.
(GETH ) GENENTECH INC.
Watch ''.rity 48.2%;
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                                                                                                                         Best Local Similarity 48.2%;
RESULT 590
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                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 48.2%;
RESULT 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human PRO polypeptide #253.
US2003207373-A1.
                                                                                                                                                                                                                                     06-NOV-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity
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                      RESULT
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ADN39242 standard; protein; 250 AA.
Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:560.
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Novel human secreted and transmembrane protein PRO1279.
US2003087357-A1.
                                                                                                                                                                 Novel human secreted and transmembrane protein PRO1279.
US2003207388-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADN16714 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003087385-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADNI5533 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279
US2003087356-A1.
ADI65156 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003207386-A1.
06-NOV-2003.
(GETH) GENENTECH INC.
45.0%; Score 618.5; DB 7; Lengtery Local Similarity 48.2%; Pred. No. 8.7e-40;
                                                                                                                                                                                                                                                                                          Aunoably standard, protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003207377-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADM82686 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003087355-A1.
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Novel human secreted and transmembrane protein PRO1279.
US2003087353-A1.
                                                                                                                                                                                                                                                                                                                                                                                                           45.0%; Score 618.5; DB 7; 48.2%; Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
                                                                                                                                                                                                                                                   DB 7;
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Pred. No. 8.7e-40;
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(EOSB-) EOS BIOTECHNOLOGY INC.
(EOSB-) EOS BIOTECHNOLOGY INC.
(45.0%; Score 618.5; DB 7
(ery Match 48.2%; Pred. No. 8.7e-40;
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Best Local Similarity 48.2%; Pred. No. 8.7e-40;
                                                                                                                                                                                                                                                 Score 618.5; DB 7
Pred. No. 8.7e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45.0%; Score 618.5; DB 748.2%; Pred. No. 8.7e-40;
                                                                                                                                                           protein; 250 AA.
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08-MX-2003.
(GETH ) GENENTECH INC.
45.0%;
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Best Local Similarity 48.2%;
RESULT 600
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                                                                                                                                                                                                                 06-NOV-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-MAY-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                    06-NOV-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 606
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                                                                                                                Best Local Similarity
RESULT 599
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
RESULT 602
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RESULT 605
                                                                                                                                                           ADH82069 standard;
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Novel human secreted and transmembrane protein PRO1279,
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                                                                                   DB 7; Length 250;
                                                                                                                                                                                                                                                                                                                                                        DB 8; Length 250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 618.5; DB 8; Length 250;
Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
                                                                                                                                                                                                                       Length 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 250;
                                                                                                                                                                                                                                                                 ADC81243 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003092115-A1.
15-MAY-2003.
(GETH ) GENENTECH INC.
ADI63655 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003207387-A1.
                                                                                                                                ADC48889 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279
                                                                                                                                                                                                                                                                                                                                                                                                     ADE21060 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279
US2003100735-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADD75879 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003100717-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADD85111 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003100722-A1.
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Pred. No. 8.7e-40;
                                                                                                                                                                                                                      DB 8;
                                                                                                                                                                                                                      Score 618.5; DB 8 Pred. No. 8.7e-40;
                                                                                                                                                                                                                                                                                                                                                     45.0%; Score 618.5; DB 8 48.2%; Pred. No. 8.7e-40;
                                                                                     Score 618.5; DB 7
Pred. No. 8.7e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADE05904 standard; protein; 250 AA. Human PRO polypeptide #93. US2003100728-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADD76691 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003100087-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADD75133 standard, protein, 250 AA Human PRO polypeptide #93. US2003100712-A1. 29-MAY-2003. (GETH ) GENENTECH INC.
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Local Similarity 48.2%;
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RESULT 616
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Local Similarity 48.2%;
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Best Local Similarity 48.2%;
RESULT 615
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(GETH ) GENENTECH INC.
                                                  06-NOV-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC
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(GETH ) GENENTECH INC
                                                                                 Query Match
Best Local Similarity
RESULT 608
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                                                                                                                                                                 US2003092888-A1.
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RESULT 610
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Length 250;
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Pred. No. 8.7e-40;
                                           Length 250;
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                                                                         AUSZU0314 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
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Novel human secreted and transmembrane protein PRO1279.
29-MAY-2003.
                                                                                                                                                                                                      ADE39111 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
                                                                                                                                                                                                                                                                             Score 618.5; DB 8;
Pred. No. 8.7e-40;
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Human secreted/transmembrane PRO polypeptide #104
                                                                                                                                                              Score 618.5; DB 8;
Pred. No. 8.7e-40;
                                            Score 618.5; DB 8;
Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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US2003203440-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADE05658 standard; protein; 250 AA.
Human PRO polypeptide #93.
US2003100727-A1.
                                                                                                                                                                                                                                                                                                                             protein; 250 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADD73643 standard; protein; 250 AA.
Human PRO polypeptide #93.
US2003100711-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         250 AA
                                                                                                                              PD 29-MAY-2003.

PA (GETH ) GENENTECH INC.

QUETY MATCh 45.0%;

Best Local Similarity 48.2%;

RESULT 618
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RESULT 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45.0%;
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RESULT 624
                                         45.0%;
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Best Local Similarity 48.2%;
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                                                                                                                                                                                                                                                                                                                                         Human PRO polypeptide #253
US2003100738-A1.
29-MAY-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                .052003096362-A1.
22-MAY-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                     15-MAY-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                                                                                                                                            30-OCT-2003.
(GETH ) GENENTECH INC.
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                                                 Best Local Similarity
RESULT 617
ID ADE20814 standard; pr
DB Novel human secreted
PD US2003100734-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity RESULT 621
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Query Match 45.0%;
Best Local Similarity 48.2%;
RESULT 642
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                                            48.28;
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(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-MAY-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
29-MAY-2003.
(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 638
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                                       Best Local Similarity
RESULT 635
                                                                                                                                                      Query Match
Best Local Similarity
RESULT 636
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Best Local Similarity
RESULT 639
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(GETH ) GEN
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                                 Query Match
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Pred. No. .8.7e-40;
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Pred. No. 8.7e-40;
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                                                Score 618.5; DB 8; Length 250;
Pred. No. 8.7e-40;
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                                                                                                                                                                              8; Length 250;
                                                                                                                                                                                                                                                                                                       DB 8; Length 250;
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Novel human secreted and transmembrane protein PRO1279.
US2003100718-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADBS5617 standard, protein, 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003100721-A1.
                                                                                                                                                                                                                                                                                                                                           ADD77421 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003100732-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADE20568 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003100733.Al.
29-MAY-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                            ADE21306 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003100736-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 45.0%; Score 618.5; DB 8; Best Local Similarity 48.2%; Pred. No. 8.7e-40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADD7149 standard; protein; 250 AA. Human PRO polypeptide #93. US2003100708-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADD74395 standard; protein; 250 AA.
Human PRO polypeptide #93.
US2003100709-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADD75633 standard; protein; 250 AA.
Human PRO polypeptide #93.
US2003100064-A1.
                                                                                              ADE23483 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003092108-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45.0%;
                                                   45.0%;
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Best Local Similarity 48.2%;
RESULT 631
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                                                            15-MAY-2003.
(GETH ) GENENTECH INC.
Query Match
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC
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                   29-MAY-2003.
(GETH ) GENENTECH INC
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Best Local Similarity
RESULT 634
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RESULT 632
                                                               Best Local Similarity RESULT 626
                                                                                                                                                                                         Best Local Similarity RESULT 627
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Best Local Similarity
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      US2003100497-A1.
                                                                                                                                                                                                                                                                           29-MAY-2003
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                                                     Query Match
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RESULT 628
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Score 618.5; DB 8; Length 250; Pred. No. 8.7e-40;
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 Length 250;
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Novel human secreted and transmembrane protein PRO1279.
US2003100731-A1.
29-MAY-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADD76923 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003100715-A1.
29-MAY-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADD86691 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279
US2003100719-A1.
Score 618.5; DB 8;
Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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                                                                                                                                                   Score 618.5; DB 8 Pred. No. 8.7e-40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 618.5; DB 8 Pred. No. 8.7e-40;
                                                                                                                                                 DB
                                                                                                                                                                                                                                                                                      PA (USIN) CLAIR 45.0%; SCOTE 61.18

Query Match
Best Local Similarity 48.2%; Pred. No RESULT 637

ID ADD87503 standard; protein; 250 AA.
DE Human PRO POLYPEPtide #253.
PN US2003203439-AI.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
AF.0%; Score 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADE89369 standard; protein; 250 AA. Human PRO polypeptide #253. US2003199062-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADE05166 standard; protein; 250 AA.
Human PRO polypeptide #93.
US2003100726-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADD75379 standard; protein; 250 AA.
Human PRO polypeptide #93.
US2003100714-A1.
                                                       ADE24035 standard; protein; 250 AA. Human PRO polypeptide #253. US2003092110-A1. 15-MAY-2003. (GETH ) GENENTECH INC.
                                                                                                                                                                                                      ADE24678 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003092111-A1.
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) 23-OCT-2003.
. (GETH ) GENENTECH INC.
Query Match 45.0%; Score 618.5; DB 8; Length 250;
                                                                                                                                    Length 250;
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Score 618.5; DB 8; Length 250;
Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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8
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Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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                                                                                                                                      Score 618.5; DB 8
Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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Human secreted/transmembrane protein PRO1279.
                                                                                                                                                                                                                                                                                                                        ADE96543 standard; protein; 250 AA.
Human secreted/transmembrane protein PRO1279.
US2003195347-A1.
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US2003199675-A1.
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1022003199061-A1.
                                                     protein; 250 AA
                                                                                                                                                                                    ADD74887 standard; protein; 250 AA.
Human PRO polypeptide #93.
US2003100724-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADF25854 standard; protein; 250 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADE95389 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003199052-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                250 AA
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 45.0%;
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23-CGT-2003.
(GETH ) GENENTECH INC.
45.0%;
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RESULT 657
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RESULT 660
                                                                                                                                    45.0%;
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Best Local Similarity 48.2%;
RESULT 655
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Human PRO polypeptide #253.
US2003199027-A1.
23-OCT-2003.
(GETH ) GENENTECH INC.
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Human PRO polypeptide #253.
US2003199060-A1.
                                                                   Human PRO polypeptide #93.
US2003100723-A1.
                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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              Best Local Similarity RESULT 653
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Best Local Similarity
RESULT 658
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RESULT 659
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Best Local Similarity
RESULT 654
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                                                 ADE05412 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US2003198993-A1.
                                                                                                      29-MAY-2003
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   Query Match
                   Score 618.5; DB 8; Length 250;
Pred. No. 8.7e-40;
                                                                                                                                                    Score 618.5; DB 8; Length 250; Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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                                                                                                                                                                                                                                                                                                              Novel human secreted and transmembrane protein PRO1279. US2003100729-A1. 29-MAY-2003. (GFH) GENERTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADD77913 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003100730-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADD85371 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279
US2003100725-AI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADD77169 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003100716-A1.
29-MAY-2003.
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Novel human secreted and transmembrane protein PRO1279.
US2003100720-AI.
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Pred. No. 8.7e-40;
                                                                                                                                                                                         Luman PRO polypeptide #253.
US2003199054-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADD73903 standard; protein; 250 AA.
Human PRO polypeptide #93.
US2003100710-A1.
                                                                 ADB18508 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003194794-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADD74641 standard; protein; 250 AA. Human PRO polypeptide #93. US2003100713-A1.
              45.0%;
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                                                                                                                                                      45.0%;
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Local Similarity 48.2%;
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Local Similarity 48.2%;
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RESULT 649
                                                                                                                                                                                                                                                                                                                                                                                                                               Watch 45.0%; Local Similarity 48.2%;
                                   48.28;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
   (GETH ) GENENTECH INC.
                                                                                                                        16-OCT-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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                                                                                                                                                                  Local Similarity
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               Query Match
Best Local Similarity
RESULT 644
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                                                                                                                                                      Query Match
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Best Loca RESULT 647

Best RESULT

BESE

A B E E E

Best Loca RESULT 648

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Query Match
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Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 668
                                                                                                                                   Length 250;
                                                                                                                                                                                                                                                                                   Length 250;
                                                                                                                                                                                                                                                                                                                                                                                                                                  45.0%; Score 618.5; DB 8; Length 250; 48.2%; Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADE92395 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003199051-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADE91843 standard, protein, 250 AA.
Novel human secreted and transmembrane protein PRO1279
US2003199058-A1.
                                                                                                                                                                                                                                                                                  45.0%; Score 618.5; DB 8; 48.2%; Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
     48.2%; Pred. No. 8.7e-40;
                                                                                                                                     Score 618.5; DB 8 Pred. No. 8.7e-40;
                                      ADF29489 standard; protein; 250 AA.
Human secreted/transmembrane protein PRO1279.
US2003203401-A1.
                                                                                                                                                                                                                                                                                                                                      ADE97020 standard; protein; 250 AA.
Human secreted/transmembrane protein PRO1279.
US2003195334-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADE90696 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003199063-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADG27253 standard; protein; 250 AA.
Human PRO polypeptide #93.
US2003096962-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADG02422 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003207352-Al.
                                                                                                                                                                                           protein; 250 AA
                                                                                                                                   Query Match
Best Local Similarity 48.2%;
RESULT 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best_Local Similarity 48.2%;
RESULT 667
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Local Similarity 48.2%;
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Best Local Similarity 48.2%;
RESULT 670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45.08;
                                                                                                                                                                                     ADF35080 standard; protein;
Human PRO polypeptide #253.
US2003199029-A1.
                                                                                                                                                                                                                                               23-OCT-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                30-OCT-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
Best Local Similarity RESULT 662
                                                                                                                                                                                                                                                                                               Best Local Similarity RESULT 664
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RESULT 666
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RESULT
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Length 250;
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Pred. No. 8.7e-40;
                                                                                                    Length 250;
                                                                                                                                                                                                                                                              DB 8; Length 250;
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ADG22208 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003207360-A1.
06-NOV-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADG24401 standard; protein; 250 AA.

Novel human secreted and transmembrane protein PRO1279.
US2003207426-A1.
06.NOV-2003.
(GETH ) GENENTECH INC.
45.0%; Score 618.5; DB 8; Lengt st Local Similarity 48.2%; Pred. No. 8.7e-40;
                                                                                                                                                                                                                                                                                                ID ADF98184 standard; protein; 250 AA.

ID ADF98184 standard; protein; 250 AA.

DE Human PRO polypeptide #253.

PN US2003207422-A1.

PA (GETH) GENENTECH INC.

Query Match

Best Local Similarity 48.2%; Pred. No. 8.7e-40;

RESULT 674
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Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 618.5; DB 8;
Pred. No. 8.7e-40;
                                                                                                                                                                                                                                                              Score 618.5; DB 8 Pred. No. 8.7e-40;
                                                                                                      Score 618.5; DB 8 Pred. No. 8.7e-40;
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                                                                                                                                                             ADG20278 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003207376-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADF98755 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003208055-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADG03586 standard; protein; 250 AA.
Human PRO polypeptide #253.
US200320731-A1.
G6-NOV-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein; 250 AA.
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US2003207375-A1.
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                                                                                                Best Local Similarity 48.2%;
RESULT 672
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Best Local Similarity 48.2%;
RESULT 673
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Best Local Similarity 48.2%;
RESULT 676
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Best Local Similarity 48.2%;
RESULT 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADF99307 standard; protein;
Human PRO polypeptide #253.
US200320733-A1.
06-NOV-2003.
(GETH ) GENENTECH INC.
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US2003207359-A1.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 680
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RESULT 675
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Human PRO polypeptide #253.
                                                                             Query Match
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                                                                                             Score 618.5; DB 8; Length 250;
Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
                                                                                                                                     Novel human secreted and transmembrane protein PRO1279.
US2009096967-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADG08512 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003207424-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADG12095 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003096963-A1.
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Novel human secreted and transmembrane protein PRO1279.
US2003207389-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ID ADGIS682 standard; protein; 250 AA.

DB Human PRO polypeptide #253.

PD 27-NOV-2003.

PA (GETH ) GENENTECH INC.

Query March

Best Local Similarity 48.2%; Pred. No RESULT 685
                                                                                                                                                                                                                                                                                                      ADG13455 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003207357-A1.
ADG19618 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003207425-A1.
06-NOV-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADF97080 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003207371-A1.
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Human PRO polypeptide #253.
US2003207374-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADG04138 standard; protein; 250 AA
                                                                                               45.0%;
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Best Local Similarity 48.2%;
RESULT 682
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Local Similarity 48.2%;
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Best Local Similarity 48.2%;
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Local Similarity 48.2%;
                                                                                                                                                                                                             22-MAY-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC
                                                                                       Query Match
Best Local Similarity
RESULT 681
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RESULT 684
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Best Local S
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Length 250;
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                                                                                                                                                                                                                                                                                                            Length 250;
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Pred. No. 8.7e-40;
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                                                                                                                                                                                                    Aury4652 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADG07888 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PR01279.
US2003207356-A1.
06-NOV-2003.
(GETH ) GENENTECH INC.
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Novel human secreted and transmembrane protein PRO1279.
                                                                                                                                                                                                                                                                                                                                                                  ADG07336 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADG55383 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003194778-A1.
                                                                   ADG25039 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279
US2003207427-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADG61047 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003207390-A1.
                                                                                                                                                                Score 618.5; DB 8;
Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
               Score 618.5; DB 8;
Pred. No. 8.7e-40;
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Best Local Similarity 48.2%; Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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Human secreted/transmembrane protein PR01279.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADG06748 standard; protein; 250 AA.
Human PRO polypeptide #93.
US2003096966-A1.
22-MAY-2003.
               45.0%;
                                                                                                                                                          Best Local Similarity 48.2%;
RESULT 691
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PA (GETH ) GENENTECH INC.
QUETY MATCh
Best Local Similarity 48.2%;
RESULT 692
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RESULT 693
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
GENENTECH INC
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Best Local Similarity
RESULT 695
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Best Local Similarity
RESULT 696
                              Best Local Similarity
RESULT 690
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RESULT 694
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Length 250;

DB 8;

Length 250;

Length 250;

Length 250;

Length 250;

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Score 618.5; DB 8; Length 250; Pred. No. 8.7e-40;
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Novel human secreted and transmembrane protein PRO1279.
US2003207419-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADG52551 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003207414-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADG54279 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003207416-A1.
                                                                                    ADG58143 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003207363-A1.
                                                                                                                                                                                                                           ADG53727 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003207415-A1.
                                                                                                                                                                                                                                                                                                                                                                              ADG71613 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003207421-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 618.5; DB 8;
Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 618.5; DB 8;
Pred. No. 8.7e-40;
                                                                                                                                                                               Score 618.5; DB 8;
Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
 22-MAY-2005.
(GETH ) GENENTECH INC.
rry Match 45.0%; Score 618.5; DB 8;
rrann Similarity 48.2%; Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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US2003207805-A1.
Sr Nov-2003.
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192003077723-A1.
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Human PRO polypeptide #253.
US2003194793-A1.
                                                                                                                                                                             45.0%;
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48.2%;
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Best Local Similarity 48.2%;
                                                                                                                                         06-NOV-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                            GENENTECH INC.
                                               Best Local Similarity RESULT 708
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Best Local Similarity
RESULT 713
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RESULT 710
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RESULT 712
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RESULT 715
22-MAY-2003
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(GETH ) GEN
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                                                 Score 618.5; DB 8; Length 250;
Pred. No. 8.7e-40;
                                                                                                                                                                                                    DB 8; Length 250;
                                                                                                                                                                                                                                                                                                                                            Score 618.5; DB 8; Length 250;
Pred. No. 8.7e-40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 8; Length 250;
                                                                                                                                                                                                                                                                                                                                                                                         ADG57039 standard; protein; 250 AA.

Novel human secreted and transmembrane protein PRO1279.
US2003207364-A1.
06-NOV-2003.
(GETH) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADH39092 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003096965-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADG55935 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003207365-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADCS8695 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003207368-A1.
06-NOV-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADG71061 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003207420-A1.
06-NOV-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                   ADG57591 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279
US2003207362-A1.
06-NOV-2003.
(GETH ) GENENTECH INC.
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Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADH04012 standard; protein; 250 AA.
Human secreted/transmembrane protein PRO1279.
US2003220471-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADH03535 standard; protein; 250 AA.
Human secreted/transmembrane protein PRO1279.
US2003224478-A1.
(GETH ) GENENTECH INC.
                                                                                                    ADG82352 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003207358-A1.
                                                                                                                                                                                                                                                                                                                                              45.0%;
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PA (GETH ) GENENTECH INC.
Query Match 45.0%;
Best Local Similarity 48.2%;
RESULT 703
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                                                  45.0%;
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RESULT 702
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RESULT 707
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RESULT 701
ID ADG57039 standard; prc
DE Novel human secreted a
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
               20-NOV-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC
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Best Local Similarity
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RESULT 705
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                                                                   Local Similarity
US2003216562-A1.
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                                                      Query Match
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Best Local &
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                                                                                        RESULT 699
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Length 250;

Length 250;

Length 250;

DB 8;

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D ADH04489 standard, protein, 250 AA.

Human secreted/transmembrane protein PRO1279.

US2004005626-A1.

OB-JAN-2004.

A (GETH ) GENENTECH INC.

Query Match

45.0%; Score 618.5; DB 8; Length 250;
45.0%; Score 618.5; DB 8; Length 250; 48.2%; Pred. No. 8.7e-40;
                                                                                                                                              Score 618.5; DB 8; Length 250;
Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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                                                   ADG56487 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003207366-A1.
06-NOV-2003.
                                                                                                                                                                                                ADH12753 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003207378-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADG54831 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279
US2003207367-A1.
06-NOV-2003.
(GETH ) GENENTECH INC.
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Novel human secreted and transmembrane protein PRO1279.
US2003207369-A1.
                                                                                                                                                                                                                                                                                                                                              ADG61599 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279
US2003207429-A1.
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Novel human secreted and transmembrane protein PRO1279
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Pred. No. 8.7e-40;
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Human PRO polypeptide #104.
US2003224984-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADH28686 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003022331-A1.
                                                                                                                                            45.0%;
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Best Local Similarity 48.2%;
RESULT 721
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Best Local Similarity 48.2%;
RESULT 723
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 722
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Best Local Similarity
RESULT 719
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               Best Local Similarity
RESULT 717
                                                                                                                                                          Best Local Similarity RESULT 718
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                                                                                                                                                                                                                                                       06-NOV-2003
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 Query Match
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Score 618.5; DB 8; Length 250; Pred. No. 8.7e-40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADG10038 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279, US2004000548-A1.
15-JAN-2004.
(GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADI14841 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003207383-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADI29907 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003096961-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADIIS509 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003207382-A1.
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Pred. No. 8.7e-40;
Best Local Similarity 48.2%; Pred. No. 8.7e-40; RESULT 726. 4.
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Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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Human secreted/transmembrane protein PRO1279.
US2004014130-A1.
                                                                                                                                                                               AD133652 standard; protein; 250 AA.
Human PRO polypeptide #93.
US2003096960-A1.
                                                                                                                                                                                                                                                                                                                      ADH69746 standard; protein; 250 AA.
Human PRO polypeptide #93.
US2004019183-A1.
29-JAN-2004.
                                    LI /26 2. ADIBLOSS standard; protein; 250 AA. Human PRO polypeptide #253. US2003207361-Al.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                               06-NOV-2003.
(GETH ) GENENTECH INC.
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                                                                                                                                            Best Local Similarity RESULT 727
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RESULT 729
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Best Local Similarity
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Best Local Similarity
RESULT 733
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Length 250;
                                                                                                                                                                                                                   Query Match 45.0%; Score 618.5; DB 8; Length 250; Best Local Similarity 48.2%; Pred. No. 8.7e-40; RESULT 737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 45.0%; Score 618.5; DB 8; Length 250;
Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 618.5; DB 8; Length 250; Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 250;
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                                                                                                                                                                                                                                                                                                                                                                Score 618.5; DB 8; Length 250;
Pred. No. 8.7e-40;
                                                                                              Length 250;
             ADI18436 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003207349-A1.
                                                                                                                                                                                                                                                                              ADJ63717 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2004039164-A1.
26-FES-2004.
(GETH ) GENENTECH INC.
                                                                                                                                             ADM27304 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279, US2004044179-A1.
04-MAR-2004.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 618.5; DB 8;
Pred. No. 8.7e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45.0%; Score 618.5; DB 8; 48.2%; Pred. No. 8.7e-40;
                                                                                               ..
8
                                                                                              Score 618.5; DB 8;
Pred. No. 8.7e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 618.5; DB 8 Pred. No. 8.7e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADK82986 standard, protein, 250 AA.
Human PRO polypeptide #104.
US2004043927-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADK66662 standard; protein; 250 AA.
Human PRO polypeptide #93.
US2004044180-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADJ65734 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2004038335-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                 ADJ77612 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2004038336-AI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADM27870 standard; protein; 250 AA Human PRO polypeptide #253.
US2004048333-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADM42594 standard; protein; 250 AA
Human PRO polypeptide #253.
US2004058424-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 48.2%; Pr
RESULT 743
ID ADMA2594 standard; protein; 250
DE Human PRO polypeptide #253.
PN US2000468424-A1.
PD 25-WAR-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45.0%;
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Best Local Similarity 48.2%;
RESULT 744
                                                                                               45.0%;
                                                                                                                                                                                                                                                                                                                                                                  Query Match 45.0%;
Best Local Similarity 48.2%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-FEB-2004.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-MAR-2004.
(GETH ) GENENTECH INC.
                                                              06-NOV-2003.
(GETH ) GENENTECH INC
                                                                                              Query Match
Best Local Similarity
RESULT 736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity RESULT 740
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SULT 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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RESULT 735
ID ADI184
DE Novel
PN US2003
PD 06-NOV
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RESULT 738
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ADR72890 standard; protein; 250 AA.
Human ovarian cancer-related tumour marker kallikrein 11 (hK11) protein2.
WO2004075713-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADR72632 standard; protein; 250 AA.

Human renal cell carcinoma-related kallikrein 11 (hK11) protein 2.

Human renal cell carcinoma-related kallikrein 11 (hK11) protein 2.

Human renal cell carcinoma-related kallikrein 11 (hK11) protein 2.

Human renal cell carcinoma-related kallikrein 11 (hK11) protein 2.

Human renal cell carcinoma-related kallikrein 11 (hK11) protein 2.

Human renal cell carcinoma-related kallikrein 11 (hK11) protein 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 618.5; DB 3; Length 282; Pred. No. 9.9e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 282;
                                                                                                          Length 250;
                                                                                                                                                                                                                                                                                   Length 250;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AD196490 standard; protein; 250 AA.
Novel human secreted and transmembrane protein PRO1279.
US2003207354-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADS34892 standard; protein; 250 AA.
Human autoimmune disease-related protein - SEQ ID 106.
WQ2004093403-A2.
(APPL-) APPLERA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY42439 standard; protein; 282 AA.
CASB12 amino acid sequence.
30-SEP-1999.
(SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
ery Match
st. Local Similarity 48.2%; Pred. No. 9.9e-40;
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(MOUN ) MOUNT SINAI HOSPITAL.

(MOUN ) MOUNT SINAI HOSPITAL.

45.0%; Score 618.5; DB 8;

HELY MATCH

48.2%; Pred. NO. 8.7e-40;
                                                                                                          45.0%; Score 618.5; DB 8; 48.2%; Pred. No. 8.7e-40;
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Pred. No. 8.7e-40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB11712 standard; protein; 282 AA.
Human serine protease BSSP6 (hBSSP6) SEQ ID NO:2.
WO200031257-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 8;
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Best Local Similarity 48.2%; Pred. No. 8.7e-40;
RESULT 751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45.0%; Score 618.5; DB 8 48.2%; Pred. No. 8.7e-40;
                                                                                                                                                                                                                                                                                 Score 618.5; DB 8
Pred. No. 8.7e-40;
ADL94689 standard; protein; 250 AA.
Human secreted/transmembrane protein PRO1279.
US2004073015.Al.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                   AD195938 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2003077659-A1.
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                                                                                                                                                                          ADM28456 standard; protein; 250 AA.
Human PRO polypeptide #253.
US2004077064-A1.
                                                                                                                                                                                                                                                                                                                                                                                                         USACOCCO
24-APR-2003.
(GETH ) GENENTECH INC.
45.0%;
                                                                                                                                                                                                                                                                                     45.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 48.2%; RESULT 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-JUN-2000.
(FUSO ) FUSO PHARM IND LID
                                                                                                                                                                                                                                              22-APR-2004. (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-NOV-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
RESULT 750
                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
RESULT 746
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                                                                                                             Query Match
Best Local Similarity
RESULT 745
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RESULT 749
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Best Local Similarity
RESULT 752
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Human secreted polypeptide #252.
US2004110939-A1.
10-UN-2004.
(GEST) GENSET SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ORTH ) ORTHO-MCNEIL PHARM RES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein; 320 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU79390 standard; protein; 256 AA Novel human kallikrein KLK15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human protease, PRTS-3 protein. WO200208396-A2.
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02-UNN-2000.

(FUSO ) FUSO PHARM IND LTD.

43.7%;

lery Match 43.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43.6%;
46.4%;
                                                                                                                                                                                            43.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-SEP-2002.
(CURA-) CURAGEN CORP.
                                                                Best Local Similarity
RESULT 763
ID ADP19401 standard; p
DE Human secreted polyp
PN US2004110339-A1.
PD 10-JUN-2004.
PA (GEST ) GENSET SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity RESULT 769
                                                                                                                                                                                                         Best Local Similarity
RESULT 764
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Best Local Similarity
RESULT 765
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE19166 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                             03-JAN-2002.
(SUGE-) SUGEN INC.
                  24-JUN-1999.
(GEST: ) GENSET.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200214485-A2.
21-FEB-2002.
 WO9931236-A2.
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Best Local S:
RESULT 770
                                                       Query Match
                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADR72889 standard; protein; 282 AA.
Human ovarian cancer-related tumour marker kallikrein 11 (hK11) protein1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB36482 standard; protein; 288 AA.
Pusion gene with human serine protease catalytic domain protein #13.
WO200066709-A2.
                                                                                                                                                                                                                                                                                                                                                                                                    ADR72631 standard; protein; 282 AA.
Human renal cell carcinoma-related kallikrein 11 (hKl1) protein 1.
WO2007060-A2.
10-SEP-2004.
(MOUN ) MOUNT SINAL HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAX42440 standard; protein; 281 AA.
CASB12 polypeptide derived from Expressed Sequence Tag products.
W09949055-A1.
                                                                     Length 282;
                                                                                                                                                                                                             Length 282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-SEP-1999.
(SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
(SMIK) SMITHKLINE A4.6%; Score 612.5; DB 2; Length 281;
(ery Match 44.6%; Score 612.5; DB 2; Length 281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45.0%; Score 618.5; DB 8; Length 282; 48.2%; Pred. No. 9.9e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 8; Length 282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45.0%; Score 618.5; DB 8; Length 282; 48.2%; Pred. No. 9.9e-40;
                                                                                                                                                                                                                                                                                                                                                     Length 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4; Length 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB67542 standard; protein; 288 AA.
Amino acid sequence of catalytic domain in PFEK1-6XHIS-TAG.
WO200116289-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY36093 standard; protein; 250 AA.
Extended human secreted protein sequence, SEQ ID NO. 478.
                                                                                                                                                                                                                                                           ADD17587 standard; protein; 282 AA.
Human soft tissue sarcoma-upregulated protein - SEQ ID . W02004048938-A2.
10-JUN-2004.
(PROT-) PROTEIN DESIGN LABS INC.
ery Match
st Local Similarity 48.2%; Pred. No. 9.9e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADS34893 standard; protein; 282 AA.
Human autoimmune disease-related protein - SEQ ID 107.
WO2004083403-A2.
A human prostate-associated serum protease (PRASP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WGCCCCCOO.

(ORTH ) ORTHO-MCNEIL PHARM RES INC.

(ORTH ) ORTHO-MCNEIL PHARM RES INC.

43.9%; Score 602.5; DB 3;

ery Match

ery Match 51.1%; Pred. No. 1.7e-38;
                                                                     Score 618.5; DB 3;
Pred. No. 9.9e-40;
                                                                                                                                                                                                               DB 8;
                                                                                                                     ADNI1325 standard; protein; 282 AA.
Human kallikrein-11, marker for prostate cancer.
WO2004029616-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45.0%; Score 618.5; DB 8 48.2%; Pred. No. 9.9e-40;
                                                                                                                                                                                                             45.0%; Score 618.5; DB 8 48.2%; Pred. No. 9.9e-40;
                                                                                                                                                                          08-APR-2004.
(MOUN ) MOUNT SINAI HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MOUN ) MOUNT SINAI HOSPITAL.
                                                                   45.0%;
                                                   (INCY-) INCYTE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-SEP-2004.
(APPL-) APPLERA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
RESULT 761
                                                                                                                                                                                                                          Best Local Similarity
RESULT 755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity RESULT 757
                                                                                Best Local Similarity
RESULT 754
                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
RESULT 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
RESULT 758
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                                    19-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-SEP-2004
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RESULT 759
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                                                                                                                                                                                                                                                                                                                                                                                                          ABREE
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AAB36483 standard; protein; 289 AA.
Fusion gene with human serine protease catalytic domain protein #14.
WO200066709-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PD 31-JAN-2002.

PA (INCY-) INCYTE GENOMICS INC.

Query Match 43.6%; Score 599.5; DB 5; Length 320;

Best Local Similarity 46.4%; Pred. No. 3.3e-38;
  Length 250;
                                                                                                                                                                                  Length 250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 320;
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                                                                                                                                                                                                                                                                                                                                                              Length 275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 225;
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Amino acid sequence of catalytic domain in PFEK1-6XHIS-TAG.
WO200116289-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 256;
43.8%; Score 601.5; DB 2; 47.4%; Pred. No. 1.8e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 43.6%; Score 598.5; DB 3; Best Local Similarity 49.1%; Pred. No. 3.5e-38; RESULT 771
                                                                                                                                                                                  DB 8;
                                                                                                                                                                                                                                            AAB11714 standard; protein; 275 AA.
Human serine protease BSSP6 (hBSSP6) SEQ ID NO:6.
WO200031257-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5
                                                                                                                                                                                                                                                                                                                                                                                                          Amino acid sequence of novel human protease #31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADN10932 standard; protein; 256 AA.
Human kallikrein 15, marker of endocrine cancer.
WO20049285-A2.
08-APR-2004.
(MOUN ) MOUNT SINAI HOSPITAL.
                                                                                                                                                                                Score 601.5; DB 8
Pred. No. 1.8e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 599.5; DB 5
Pred. No. 3.3e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43.6%; Score 599; DB 5; 49.8%; Pred. No. 2.5e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43.6%; Score 599; DB 8; 47.1%; Pred. No. 2.8e-38;
                                                                                                                                                                                                                                                                                                                                                           Score 601; DB 3;
Pred. No. 2.1e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43.6%; Score 599; DB 5; 47.1%; Pred. No. 2.8e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADI17075 standard; protein; 225 AA.
Murine NOVX protein homologue SeqID 611.
WO200268649-A2.
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Length 251;

BBBBB

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41.4%; Score 569.5; DB 3; 46.9%; Pred. No. 5.2e-36;
                                            (MOUN ) MOUNT SINAI HOSPITAL.
                                                                              Query Match
Best Local Similarity
RESULT 781
                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
RESULT 782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
RESULT 787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
RESULT 785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-2002.
(HYSE-) HYSEQ INC.
           14-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PA (FUSO ) FUSO PHARM IND LTD.
Query Match 43.5%; Score 597.5; DB 3; Length 276;
Best Local Similarity 47.0%; Pred. No. 4e-38;
) 08-MAR-2001.

(ORTH) ORTHO-MCNEIL PHARM INC.

Query Match

Query Match

---- Similarity 49.1%; Pred. No. 3.5e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 43.2%; Score 593.5; DB 5; Length 260; Best Local Similarity 48.6%; Pred. No. 7.7e-38; RESULT 776
                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 45.6%; Pred. No. 2.8e-36; DB 8; Length 247; RESULT 780 Et andard; protein: 2.1 ABB1306 standard; protein: 2.1 WOARD ET Human Kir-L6 protein: 2.1 WOARD ET HUMAN KIR-L6 protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.1 Protein: 2.
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PA (MOUNT SINAI HOSPITAL.
Query Match 43.1%; Score 592; DB 3; Length 228;
Best Local Similarity 49.3%; Pred. No. 8.7e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43.3%; Score 595; DB 7; Length 298; 48.1%; Pred. No. 6.8e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41.7%; Score 573; DB 2; Length 247; 45.6%; Pred. No. 2.8e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB11713 standard; protein; 276 AA.
Mouse serine protease BSSP6 (mBSSP6) SEQ ID NO:4.
WQ200031257-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADC31389 standard; protein; 298 AA.
Human novel polypeptide sequence, SEQ ID NO:1471.
W0200302571_A2.
10-APR-2003.
(HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                          43.5%; Score 597.5; DB 4 47.8%; Pred. No. 3.6e-38;
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(HOFF) HOFFMANN LA ROCHE & CO AG F.

117 Match

41.7%; Score 573; DB 5;

12 Local Similarity 45.6%; Pred. No. 2.8e-36;
                                                                                                                                                                                           AAE08017 standard; protein; 248 AA.
Human PS133 consensus protein sequence.
US6232456-B1.
15-MAY-2001.
(ABBO ) ABBOTT LAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADI17077 standard; protein; 260 AA.
Human NOVX protein homologue SeqID 613.
WO200268649-A2.
(CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW08475 standard; protein; 247 AA. Porcine trypsinogen. W09700316-A1. 03-JAN.1997. (NOVO ) NOVO-NORDISK AS.
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Pig trypsinogen SEQ ID NO 1.
WO200261064-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADJ92132 standard; protein; 247 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB21312 standard; protein; 228 AA
                                                                                                        Best Local Similarity RESULT 772
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Best Local Similarity
RESULT 775
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RESULT 778
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WO200053776-A2.
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PADAGE

A D S E E

BBBBB

PN

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DE Human protein modification + maintenance molecule protein SEQ ID No 20.

BE Human protein modification + maintenance molecule protein SEQ ID No 20.

BY WO203000844-A2.

BY WO203000844-A2.

BY WO2041-A2.

BY WO2011-A2.

BEST LOCAL Similarity 46.9%; Pred. No. 5.6e-36;

BESTULT 783

ID AAB21298 standard; protein; 250 AA.

BY WO200053776-A2.

BY WO200053776-A2.

BY WO2001-A2.

BY WO2001-A3.

BY WO2001-A3.

BY WO3001-A3.

BY
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                                                                                                                                                                                                                                     Length 251;
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PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 41.3%; Score 567; DB 3; Length 277;
Best Local Similarity 46.8%; Pred. No. 9e-36;
RESULT 788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41.3%; Score 567; DB 6; Length 277; 46.8%; Pred. No. 9e-36;
                                                                                                                       MOSCOL-2004.

(MOUN ) MOUNT SINAI HOSPITAL.

(MOUN ) MAINT SINAI HOSPITAL.

41.4%; SCORE 569.5; DB 8;

LELY MAICH

41.4%; Pred. No. 5.2e-36;
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Amino acid sequence of human kallikrein 9 (hK9).
WO2003033731-A2.
ADN10930 standard; protein; 251 AA.
Human kallikrein 14, marker of endocrine cancer.
WO2004029285-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Heet Local Similarity 46.7%; Pred. No. 6.2e-36; RESULT 784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41.4%; Score 568.5; DB 5
46.7%; Pred. No. 6.2e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADL/1094 standard; protein; 277 AA.
Human Kallikrein 13 protein SEQ ID NO:1.
02004021009-A2.
11-MAR-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADNO5516 standard; protein; 250 AA.
Antipsoriatic protein sequence #924.
WO2004028479-A2.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB21300 standard; protein; 277 AA.
Human KLK-L4 protein #2.
WO200053776-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABP64969 standard; protein; 250 AA.
Human protein SEQ ID 629.
WO200259260-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABO00554 standard; protein; 277 AA. Novel human polypeptide #141. WOZO03023013-A2. 20-MAR-2003. (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-APR-2003.
(MOUN ) MOUNT SINAI HOSPITAL.
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Query Match 41.1%; Score 564.5; DB 3; Length 293; Best Local Similarity 45.3%; Pred. No. 1.5e-35; RESULT 799
                                                                                                                                                    (MOUN ) MOUNT SINAI HOSPITAL.

41.1%; Score 564.5; DB 3; Length 293; tr Local Similarity 45.3%; Pred. No. 1.5e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41.1%; Score 564.5; DB 4; Length 293; 45.3%; Pred. No. 1.5e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 41.1%; Score 564.5; DB 5; Length 293; Best Local Similarity 45.3%; Pred. No. 1.5e-35; RESULT 803
                                                                                                                                                                                                                                                                                                                                            DB 4; Length 293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-DEC-2002.
(HUMA-) HUMAN GENOME SCI INC.
(ary Match 41.1%; Score 564.5; DB 6; Length 293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41.1%; Score 564.5; DB 6; Length 293; 45.3%; Pred. No. 1.5e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 564.5; DB 6; Length 293;
Pred. No. 1.5e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human secreted and transmembrane protein PRO1132 US2003032156-A1.
                                                                                                                                                                                                                                                                                                                                                                                                AAB65249 standard; protein; 293 AA.
Human PRO1132 (UNQ570) protein sequence SEQ ID NO:309.
WO200073454-A1.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABU59142 standard; protein; 293 AA.
Novel human secreted or transmembrane protein PRO1132.
US200213222-A1.
19-SEP-2002.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 41.1%; Score 564.5; DB 6;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 6;
                                                                                                                                                                                                                                                                                                                           Query Match 41.1%; Score 564.5; DB 4
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41.1%; Score 564.5; DB 6 45.3%; Pred. No. 1.5e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABU82654 standard; protein; 293 AA.
Human secreted/transmembrane protein PRO1132.
12-03033032-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU81966 standard; protein; 293 AA.
Human PRO1132.
WO200109327-A2.
08-FEB-2001.
(GETH ) GENENTECH INC.
                                                                           AAB21296 standard; protein; 293 AA
                                                                                                                                                                                                                                          AAU12399 standard; protein; 293 AA.
                                                                                                                                                                                                                                                           Human PRO1132 polypeptide sequence. WO200140466-A2. 07-JUN-2001. (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABUS8064 standard; protein; 293 AA.
Human PRO polypeptide #96.
US2003027163-A1.
06-FEB-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein; 293 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADA57425 standard; protein; 293 AA. Human secreted protein #257. WO2002102994-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 41.1%;
Best Local Similarity 45.3%;
RESULT 807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-FEB-2003.
(GETH ) GENENTECH INC.
                                                                                              Human KLK-L2 protein.
WO200053776-A2.
14-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
RESULT 806
                                                                                                                                                                                            Best Local Similarity
RESULT 800
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Best Local Similarity
RESULT 802
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Best Local Similarity
RESULT 808
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABO17843 standard;
                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY30524 standard; protein; 293 AA.
Human PDSP-1 protein.
MO9946391-A2.
16-SEP-1999.
(MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
ery Match
st Local Similarity 45.3%; Pred. No. 1.5e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41.2%; Score 566.5; DB 4; Length 251; 46.9%; Pred. No. 8.9e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41.1%; Score 564.5; DB 2; Length 293; 45.3%; Pred. No. 1.5e-35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 293;
                                                                                                                                                                                                                                                    ADRÍ4575 standard; protein; 277 AA.

Human NF-kappaB pathway-associated protein SeqID576.
WQ2004065577-A2.
05-AUG-2004.
(BRIM ) BRISTOL-MYERS SQUIBB CO.
ery Match
st Local Similarity 46.8%; Pred. No. 9e-36;
                                   Length 277;
                                                                                                                                                                                                Length 277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-AUG-2001.
(HUWA-) HUMAN GENOME SCI INC.
(HIP; Score S64.5; DB 4;
lery Match 41.1%; Score S64.5; DB 4;
                                                                                                                                                                                          Query Match 41.3%; Score 567; DB 8; Best Local Similarity 46.8%; Pred. No. 9e-36; RESULT 791
                                   41.3%; Score 567; DB 8; 46.8%; Pred. No. 9e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41.1%; Score 564.5; DB 2 45.3%; Pred. No. 1.5e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY38426 standard; protein; 293 AA.
Human secreted protein encoded by gene No. 27.
WO9935158-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene No. 27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY16777 standard; protein; 293 AA.
Human keratinocyte derived protease (KDP).
WO9918219-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                 AAU16971 standard; protein; 251 AA.
Human novel secreted protein, SEQ ID 212.
WO200155441-A2.
                                                                                         ADN04184 standard; protein; 277 AA. Antipsoriatic protein sequence #287 WO2004028479-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU23217 standard, protein, 247 AA.
Novel human enzyme polypeptide #303
WO200155301-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY38412 standard, protein, 293 AA
Human secreted protein encoded by o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY66726 standard; protein; 293 AA. Membrane-bound protein PRO1132.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
                (MOUN ) MOUNT SINAI HOSPITAL.
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15-JUL-1999.
(HUMA-) HUMAN GENOME SCI INC.
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(PROC ) PROCTER & GAMBLE CO.
                                                                                                                                                                                                                                                                               08-APR-2004.
(GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GETH ) GENENTECH INC.
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Best Local Similarity
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Best Local Similarity
RESULT 795
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                                                Best Local Similarity RESULT 790
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RESULT 798
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A S S S S S

Length 293;

Length 293;

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Query Match
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 817
ID ADA41305 standard; protein; 293 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 41.1%; Score 564.5; DB 6; Length 293; Best Local Similarity 45.3%; Pred. No. 1.5e-35; RESULT 813
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Beet Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 815
                                                                                                41.1%; Score 564.5; DB 6; Length 293; 45.3%; Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
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Novel human secreted and transmembrane protein PRO1132 US2003003531-A1.
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Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human secreted/transmembrane protein, #130.
US2002160384-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABU13955 standard; protein; 293 AA.
Human PRO1132 polypeptide.
US2002103125-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABU81097 standard; protein; 293 AA.
Human PRO polypeptide #228.
US2003004311-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABU66797 standard, protein, 293 AA.
Human PRO polypeptide #228.
US2003036180-A1.
ADA56974 standard; protein; 293 AA.
Human secreted protein #257.
WO2002102994-A2.
                                                                                                                                                          ADAS7427 standard; protein; 293 AA.
Human secreted protein #257.
WO2002102994-A2.
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Human secreted protein.
WO2002102993-A2.
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(HUMA-) HUMAN GENOME SCI INC.
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Best Local Similarity 45.3%;
RESULT 812
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH LTD.
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(GETH ) GENENTECH INC.
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RESULT 814
                                                                                                                   Local Similarity
                                                            27-DEC-2002
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Best Local Si
RESULT 810
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RESULT 809
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Length 293;
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Pred. No. 1.5e-35;
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Novel human secreted and transmembrane protein PRO1132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABU59438 standard; protein; 293 AA.
Novel human secreted or transmembrane protein PRO1346.
US2003027985-A1.
06-FEB-2003.
                                                                                                          ID ADA40825 standard; protein; 293 AA.
DE Human secreted protein.
PN WC2002102993-A2.
PD 27-DEC-2002.
PA (HTMA-) HUMAN GENOME SCI INC.
QUETY MAtch
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
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Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 825
                                                              Query Match 41.1%; Score 564.5; DB 6; Best Local Similarity 45.3%; Pred. No. 1.5e-35; RESULT 818
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Pred. No. 1.5e-35;
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Novel secreted and transmembrane protein PRO1132
US2003017563-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABO25068 standard; protein; 293 AA.
Human secreted/transmembrane protein (PRO) #228.
US2003036179-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41.1%; Score 564.5; DB 6
45.3%; Pred. No. 1.5e-35;
                                                                                                                                                                                                                                                                                     ADM41306 standard; protein; 293 AA.
Human secreted protein.
WG2002102993-A2.
27-DEC-2002.
(HUMA-) HUMAN GENOME SCI INC.
41.1%; Score 564.5; DB 6
st Local Similarity 45.3%; Pred. No. 1.5e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABUS8995 standard; protein; 293 AA.
Human sectreted/transmembrane protein, #130.
US2002142961-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABU59289 standard; protein; 293 AA.
Human secreted/transmembrane protein, #130.
US2003027162-A1.
06-FEB-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABO25986 standard; protein; 293 AA.
Human PRO1132 polypeptide.
US2002127576-A1.
(GETH ) GENENTECH INC.
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                                                          (HUMA-) HUMAN GENOME SCI INC.
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Best Local Similarity 45.3%;
RESULT 824
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Human secreted protein. WO2002102993-A2. 27-DEC-2002.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 822
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Best Local Similarity
RESULT 821
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Best Local Similarity
RESULT 820
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ADA61679 standard; protein; 293 AA.
              Homo sapiens.
US2003049816-Al.
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Best Local S
RESULT 845
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 41.1%; Score 564.5; DB 6; Length 293; 45.3%; Pred. No. 1.5e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 41.1%; Score 564.5; DB 6; Length 293; Local Similarity 45.3%; Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
                                                                                                                                                                                                                                                                                                                                                                      DB 6; Length 293;
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                                                                                                                              Length 293
                                                                                                                                                                  ABU92204 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003017476-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                   ABU81662 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132
US2002177164-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADA45975 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132
US2003022328-A1.
                                                               Human secreted/transmembrane, PRO, protein SEQ ID 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABU88601 standard; protein; 293 AA.
Human secreted and transmembrane polypeptide PRO1132
US2002197615-A1.
                                                                                                                            Score 564.5; DB 6;
Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
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45.3%; Pred. No. 1.5e-35;
                                              protein; 293 AA.
                                                                                                                                                                                                                                                                                     ABU10910 standard; protein; 293 AA.
Human PRO polypeptide #96.
US2002123463-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABO34115 standard; protein; 293 AA Human PRO1132 polypeptide. US2003017981-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADA19056 standard; protein; 293 AA
Human PRO polypeptide #228.
US2003054517-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         293 AA
                                                                                                                            41.18;
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                                                                                                                                                                                                                                          41.1%;
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RESULT 835
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Beet Local Similarity 45.3%;
RESULT 836
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Human PRO polypeptide #228.
US2003073212-A1.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                       05-SEP-2002.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-NOV-2002.
(GETH ) GENENTECH INC
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(GETH ) GENENTECH INC.
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                                                                                                             (GETH ) GENENTECH INC
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Best Local Similarity
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             Best Local Similarity RESULT 827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                     Best Local Similarity
RESULT 829
                                                                                                                                        Best Local Similarity RESULT 828
                                                ABU67073 standard;
                                                                              US2003032155-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-JAN-2003.
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Best Local S
RESULT 833
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RESULT 830
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RESULT 831
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RESULT 832
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RESULT
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Query Match 41.1%; Score 564.5; DB 6; Length 293; Best Local Similarity 45.3%; Pred. No. 1.5e-35; RESULT 839
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                                    Score 564.5; DB 6; Length 293; Pred. No. 1.5e-35;
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                                                                                                                                                                                                                                                                                                                                                                             AUAR6484 standard; protein; 293 AA.

Novel human secreted and transmembrane protein PRO1132.
US2003082711.A1.
01-MAY-2003.
(GETH) GENENTECH INC.
                                                                           Ausiy464 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003068796-A1.
                                                                                                                                                                              Query Match
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 564.5; DB 6;
Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 564.5; DB 6;
Pred. No. 1.5e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 843
ID ADA21506 standard; protein; 293 AA.
ID Human secreted/transmembrane polypeptide PRO1132.
PD 105200305444-A1.
PD 20-MAR-2003.
41.1%; Score 564.5; DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADA10293 standard; protein; 293 AA.
Huwan secreted/transmembrane protein, PRO1132.
27-MAR-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADA37820 standard; protein; 293 AA.
Human secreted/transmembrane protein PRO1132.
US2003008297-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human PRO polypeptide #228.
US2003087350-A1.
08-MAY-2003.
SY WATCH JENEWIECH INC.
                                                                                                                                                                                                                                       ADB28005 standard; protein; 293 AA.
Human PRO polypeptide #228.
US2003082704-A1.
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Human PRO polypeptide #228.
US2003073215-A1.
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Human PRO polypeptide #228.
US2003068795-A1.
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RESULT 840
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Best Local Similarity 45.3%;
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                                    41.18;
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45.38;
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Best Local Similarity 45.3%;
13-MAR-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                 10-APR-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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                                    Query Match
Best Local Similarity
RESULT 837
ID ADB19464 standard; p.
DE Novel human secreted
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45.3%; Pred. No. 1.5e-35;

Best Local Similarity RESULT 855

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ADA91881 standard; protein; 293 AA.

Novel human secreted and transmembrane protein PRO1132.
US2003082694-A1.
01-MAY-2003.
(GETH ) GENENTECH INC.
ery Match
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                            Score 564.5; DB 6; Length 293;
Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADA87587 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003087345-A1.
                                                                                                                                                                                             ADA85932 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132
US2003082693-A1.
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Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
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45.3%; Pred. No. 1.5e-35;
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Human secreted/transmembrane protein PRO1132.
US2003054359-A1.
20-MAR-2003.
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N US2003082763-A1.

D 01-MAY-2003.

A (GETH.) GENENTECH INC.

Roch 7.
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Human PRO1132 polypeptide.
US2003054987-A1.
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Human PRO polypeptide #228.
US2003087349-A1.
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Human PRO polypeptide #228.
US2003082705-A1.
                                                                        protein; 293 AA
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45.3%;
                                                                    ADB30636 standard; protein,
Human PRO polypeptide #228.
US2003068794-A1.
10-APR-2003.
(GETH ) GENENTECH INC.
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Local Similarity 45.3%;
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Best Local Similarity 45.3%;
                               41.18;
                                             45.3%;
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(GETH ) GENENTECH INC.
10-APR-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                       Best Local Similarity RESULT 846
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Best Local Similarity
RESULT 848
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Best Local Similarity
RESULT 849
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Score 564.5; DB 6; Length 293; Pred. No. 1.5e-35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABO43376 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
06-20030449495-A1.
06-MAR-2003.
(GETH ) GENENTECH INC.
                                                                                                                         мылвур5 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003073211-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                     ADB20016 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003082691-A1.
01-MAY-2003.
(GETH ) GENENTECH INC.
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                                                                                                                                                                                                                              DB 6;
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Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
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45.3%; Pred. No. 1.5e-35;
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45.3%; Pred. No. 1.5e-35;
                                                                                      Score 564.5; DB 6
Pred. No. 1.5e-35;
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Human secreted/transmembrane protein PRO1132.
22-MAR-2003.
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Human PRO polypeptide SEQ ID NO 456
US2003077713-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADB13328 standard; protein; 293 AA. Human PRO polypeptide #228. US2003082710-A1. 01-MAY-2003 (GETH ) GENENTECH INC.
ADB14944 standard; protein; 293 AA. Human PRO polypeptide #228. US2003087351-A1.
                                                                                                                                                                                                                                                                        ADA99120 standard; protein; 293 AA. Human PRO polypeptide #228. US2003077722-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein; 293 AA
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                                                                                    Query Match 41.1%;
Best Local Similarity 45.3%;
RESULT 856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 45.3%; RESULT 860
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Best Local Similarity 45.3%;
RESULT 858
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US2003068798-A1.
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(GETH ) GENENTECH INC.
                                                      08-MAY-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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RESULT 862
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Query Match 41.1%; Score 564.5; DB 6; Length 293; Best Local Similarity 45.3%; Pred. No. 1.5e-35; RESULT 881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 879
                                                           Length 293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vuery Match 41.1%; Score 564.5; DB 6; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 880
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Pred. No. 1.5e-35;
                                                                                                                                                                                                                 Score 564.5; DB 6; Length 293;
Pred. No. 1.5e-35;
                                                                                                                                                                                                                                                                                                                                                                          6; Length 293;
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                                                           Score 564.5; DB 6;
Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 564.5; DB 6
Pred. No. 1.5e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADA92871 standard; protein; 293 AA.
Human secreted/transmembrane protein PRO1132.
22.03060407-A1.
27-MAR-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human PRO polypeptide SEQ ID NO 456. US2003077714-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALMAYO592 standard; protein; 293 AA. Human PRO polypeptide #228. US2003082690-A1. 01-MAY-2003. (GTH ) GENENTECH INC.
                                                                                                              ADA93551 standard; protein; 293 AA.
Human PRO polypeptide #228.
US2003077721-A1.
24-APR-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                         ADB26901 standard; protein; 293 AA. Human PRO polypeptide #228. US2003092147-A1. 15-MAY-2003. (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                 ADB31188 standard, protein, 293 AA.
Human PRO polypeptide #228.
US2003096386-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADA81164 standard, protein; 293 AA.
Human PRO polypeptide #228.
US2003082702-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADA61116 standard; protein; 293 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADA96040 standard; protein; 293 AA.
Human PRO polypeptide #228.
01-MXY-2003.
                                                                                                                                                                                                             Best Local Similarity 45.3%;
RESULT 875
                                                           41.1%;
                                                                                                                                                                                                                                                                                                                                                                        Query Match 41.1%;
Best Local Similarity 45.3%;
RESULT 876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41.1%;
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Best Local Similarity 45.3%;
RESULT 878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-MAY-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                        GENENTECH INC.
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Best Local Similarity
RESULT 882
                                                             Query Match
Best Lôcal Similarity
RESULT 874
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Best Local Similarity
RESULT 877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
US2003049817-A1.
    US2003077715-A1.
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 41.1%; Score 564.5; DB 6; Length 293; Best Local Similarity 45.3%; Pred. No. 1.5e-35; RESULT 867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41.1%; Score 564.5; DB 6; Length 293; 45.3%; Pred. No. 1.5e-35;
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                                                                                               Score 564.5; DB 6; Length 293; Pred. No. 1.5e-35;
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                                                                                                                                                                                                                                                                                                           ADAB5380 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003082695-A1.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADA84828 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003082708-A1.
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Human secreted/transmembrane protein PRO1132.
22.033059780-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADB25375 standard; protein; 293 AA. Human PRO polypeptide SEQ ID NO 456.
ADA82339 standard; protein; 293 AA. Human PRO polypeptide #228. US2003082701.A1. 01-MAY-2003. (GETH ) GENENTECH INC.
                                                                                                                                                      ADA75302 standard; protein; 293 AA.
Human PRO polypeptide #228.
US2003073216-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADB30084 standard, protein; 293 AA.
Human PRO polypeptide #228.
US2003073214-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADA80612 standard; protein; 293 AA.
Human PRO polypeptide #228.
US2003082761-A1.
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Human PRO polypeptide #228.
US2003082703-A1.
01-MAY-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MDA47079 standard; protein; 293 AA. Human PRO polypeptide #228.
US2003073210-Al.
                                                                                                 41.1%;
                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 45.3%;
RESULT 866
                                                                                                                                                                                                                      17-APR-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC
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(GETH ) GENENTECH INC.
                                                                                                   Query Match
Best Local Similarity
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Best Local Similarity
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Best Local Similarity
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RESULT 870
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Query Match

RESULT 872

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Human PRO polypeptide #228.
27-Man PRO polypeptide #228.
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Human PRO polypeptide #228.
US2003022239-A1.
33-JAN-2003.
                                         protein; 293
                                                                                                                                                                                                                                                                                                                41.1%;
41.1%;
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45.3%;
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45.3%;
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                                                                                                                                                                                     27-MAR-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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RESULT 895
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RESULT 896
Query Match
Best Local Similarity
RESULT 892
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Best Local Similarity
RESULT 893
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Best Local Similarity
RESULT 894
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Best Local Similarity
RESULT 898
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RESULT 899
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                                         ABO53201 standard;
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              Length 293;
                                                                                                                              DB 6; Length 293;
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Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
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Novel human secreted and transmembrane protein PRO1132.
US2003082709-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADA88139 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003082700-A1.
01-MAY-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADA46527 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003054516-A1.
                                                                                                                                                                    ADB21834 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132 US2003082765-A1.
              Score 564.5; DB 6;
Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
                                                                                                                                                                                                                                                                                 ADA77613 standard, protein, 293 AA.
Human PRO polypeptide #228.
US2003068797-A1.
                                                      ADB26349 standard; protein; 293 AA.
Human PRO polypeptide #228.
US2003082760-A1.
                                                                                                                                                                                                                                                                                                                                                                                                  ADB18353 standard; protein; 293 AA.
Human PRO polypeptide #228.
US2003077710-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein; 293 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADB29109 standard; protein; 293 AA.
Human PRO polypeptide #228.
US2003082706-A1.
                                                                                                                            41.1%;
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45.3%;
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RESULT 890
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Best Local Similarity 45.3%;
                Query Match
Best Local Similarity 45.3%;
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Human PRO polypeptide #228
US2003082699-A1.
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(GETH ) GENENTECH INC.
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Best Local Similarity 4
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(GETH ) GENENTECH INC.
                                                                                                   O 01-MAY-2003.
GETH ) GENENTECH INC.
Query Match 4
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(GETH ) GENENTECH INC.
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 (GETH ) GENENTECH INC
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RESULT 886
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RESULT
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Length 293;
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Length 293;
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Novel human secreted and transmembrane protein PRO1132.
US2003073213-A1.
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Novel human secreted and transmembrane protein PRO1132.
US2003087344-A1.
08-MAY-2003.
                                                                                                                                                                                                                                                                                             Score 564.5; DB 7;
Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
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Human secreted/transmembrane PRO polypeptide #96
US2003049638-A1.
13-MAR-2003.
                                                                                                                                                                                                                                                                                                                                                       ADA22432 standard; protein; 293 AA.
Human secreted/transmembrane polypeptide PRO1132
V320030404473-A1.
27-FEB-2003.
Score 564.5; DB 7,
Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
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Human secreted/transmembrane protein PRO1132.
US2003017982-A1.
23-JAN-2003.
                                                                          Human secreted/transmembrane protein PRO1132.
US2003044806-A1.
06-MAR-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADA39291 standard; protein; 293 AA.
Human secreted/transmembrane protein PRO1132.
22003059782-A1.
27-MAR-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human PRO polypeptide #228.
US2003082686-Al.
01-MAY-2003.
GGTH ) GENENTECH INC.
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41.1%; Score 564.5; DB 7; Length 293; 45.3%; Pred. No. 1.5e-35;
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                                                                                                                                                                                               Length 293;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADA92433 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132 US2003082712-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADB38748 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003082766-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADB38196 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003087347-A1.
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                                                                                                                                                                                             41.1%; Score 564.5; DB 7 45.3%; Pred. No. 1.5e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 564.5; DB 7
Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
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                                                                                              Human PRO polypeptide #228.
10-2003068793-A1.
                                                                                                                                                                                                                                          ADB22938 standard; protein; 293 AA.
Human PRO polypeptide #228.
US2003077711-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADB96317 standard; protein; 293 AA.
Human PRO polypeptide #96.
US2003054403-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADB15496 standard; protein; 293 AA.
Human PRO polypeptide #228.
US2003087352-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41.18;
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45.3%;
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45.38;
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(GETH ) GENENTECH INC.
Local Similarity RESULT 902
ID ADA67077 stand PN US20030 PN US20030 PN
                                                                                                                                                        10-APR-2003.
(GETH ) GENENTECH INC
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC
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Best Local Similarity
RESULT 907
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Best Local Similarity
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Best Local S
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                                                                                                                                                                                                                              RESULT 903
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vuery Match 41.1%; Score 564.5; DB 7; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 913
                                                                                                             Length 293;
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                                                                                                                                                                                                                                                                                                                                                                                                               41.1%; Score 564.5; DB 7; Length 293; 45.3%; Pred. No. 1.5e-35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADB19581 standard, protein, 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003082764-A1.
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Novel human secreted and transmembrane protein PRO1132
US2003082687-A1.
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Novel human secreted and transmembrane protein PRO1132
US2003082696-A1.
                                                                                                             Score 564.5; DB 7;
Pred. No. 1.5e-35;
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Best Local Similarity 45.3%; Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
                                                                                                                                                                                                                                                                                                                   ADB80490 standard; protein; 293 AA.
Ovarian cancer-associated protein #27.
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US200307777-A1.
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RESULT 911

ID ADB89748 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2093082698-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
                                                                                                                                                                 ADB90480 standard; protein; 293 AA. Human PRO polypeptide #228. US2003082762-A1. 01-MAY-2003 (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            293 AA
                                                                                                                                                                                                                                                                                                                                                   WO2002102235-A2.
27-DEC-2002.
(EOSB-) BOS BIOTECHNOLOGY INC.
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RESULT 917
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RESULT 919
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RESULT 912
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Best Local Similarity 45.3%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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RESULT 920
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Score 564.5; DB 7; Length 293; Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
                                                                                 Length 293;
                                                                                                                                                                                                                                                                                                                                                                                                           ADB46624 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003082692-A1.
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Pred. No. 1.5e-35;
                                                                                 Score 564.5; DB 7;
Pred. No. 1.5e-35;
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45.3%; Pred. No. 1.5e-35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADC12020 standard; protein; 293 AA.
Human secreted/transmembrane protein PRO1132.
US2003049681-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADC07497 standard; protein; 293 AA.
Human secreted/transmembrane protein PRO1132.
US2003068647-A1.
ADB34021 standard, protein, 293 AA. Human PRO polypeptide SEQ ID NO 456. US2003077716-A1.
                                                                                                                                                                                                                                                                   ADB36229 standard; protein; 293 AA. Human PRO polypeptide SEQ ID NO 456. US2003077720-A1.
                                                                                                                                  ADB35125 standard; protein; 293 AA. Human PRO polypeptide SEQ ID NO 456. US2003077718-A1.
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US2003064375-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADC57789 standard; protein; 293 AA.
Human PRO polypeptide #96.
US2003027754-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADC55153 standard; protein; 293 AA.
Human PRO polypeptide #96.
US2003045463-A1.
06-MAR-2003.
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45.3%;
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45.3%;
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45.3%;
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RESULT 923
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45.38;
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45.38;
                                                                                    41.1%;
45.3%;
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Best Local Similarity 45.38;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                    GENENTECH INC
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Best Local Similarity
RESULT 924
                                                                                                  Local Similarity
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RESULT 929
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Best Local Similarity
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Best Local Similarity
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Best Local S
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Score 564.5; DB 7; Length 293;
Pred. No. 1.5e-35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         ADC53030 standard; protein; 293 AA.
Novel human secreted and transmembrane protein Seq ID456.
08-MAY-2003.
(GETH ) GENENTECH INC.
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Novel human secreted and transmembrane protein Seg ID456.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADC57384 standard; protein; 293 AA.
Novel human secreted and transmembrane protein Seg ID456.
US2003087366-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADC60575 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PR01132.
US2033087367-A1.
08-MAY-2003.
(GETH ) GENENTECH INC.
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Novel human secreted and transmembrane protein PRO1132.
US2003087361-A1.
ADC50497 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003092106-A1.
                                                                                                                                                ADC72044 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132
US2003092107-A1.
                                                                                                                                                                                                                                                                                              ADC60023 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132
US2003092105-A1.
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Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 934
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Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 935
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Pred. No. 1.5e-35;
                                                                                        Score 564.5; DB 7
Pred. No. 1.5e-35;
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45.3%; Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
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US2003087362-A1.
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                                                                                          41.1%;
45.3%;
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Best Local Similarity 45.3%;
RESULT 932
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(GETH ) GENENTECH INC.
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                                                     15-MAY-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 937
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RESULT 936
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                                                                                              Query Match
Best Local Similarity
RESULT 931
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Length 293;
                                                                                                                                                        Score 564.5; DB 7; Length 293; Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
                  41.1%; Score 564.5; DB 7; Length 293; 45.3%; Pred. No. 1.5e-35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUDUGABS Standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
082203087354-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADD08679 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003073090-A1.
17-APR-2003.
                                                                                                                                                                                                                                                                                                                                                     ADD07608 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132
US2002193299-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel human secreted and transmembrane protein PRO1132 US2003092103-A1.
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Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
                                                        protein; 293 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein; 293 AA.
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Human PRO polypeptide #228.
US2003194774-A1.
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                                                                                                                                                    Best Local Similarity 45.3%;
RESULT 950
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RESULT 952
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45.3%;
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45.3%;
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Human PRO polypeptide #228.
US2003194771-A1.
                                                                                                                                                                                                                               Human PRO polypeptide #228.
US2003194776-Al.
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US2003059833-A1.
27-MAR-2003.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                             Best Local Similarity RESULT 949
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Best Local Similarity
RESULT 951
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RESULT 955
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                                                                                                                                                                                                             ADD10110 standard;
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                                                                                      DB 7; Length 293;
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Pred. No. 1.5e-35;
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ADC53636 standard; protein; 293 AA.
Novel human secreted and transmembrane protein Seg ID456.
US2003087364-A1.
                                                                                                                                     ADC59159 standard; protein; 293 AA.
Novel human secreted and transmembrane protein Seg ID456.
US2003087359-A1.
                                                                                                                                                                                                                                                                           ADC56037 standard; protein; 293 AA.
Novel human secreted and transmembrane protein Seg ID456.
US2003087360-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                         ADC58607 standard; protein; 293 AA.
Novel human secreted and transmembrane protein Seg ID456 US2003087346-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADC14609 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003082546-A1.
01-MAY-2003.
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Novel human secreted and transmembrane protein PRO1132
US2003068623-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADD03281 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003092104-A1.
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Novel human secreted and transmembrane protein PRO1132 US2003087348-A1.
                                                                                                                                                                                                                              Score 564.5; DB 7;
Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
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US2003083461-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADC69692 standard; protein; 293 AA. Human PRO polypeptide #228. US2003194770-A1. 16-OCT-2003.
                                                                                    41.1%;
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Best Local Similarity 45.3%;
RESULT 941
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45.3%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC
                                                                                                 Best Local Similarity RESULT 940
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RESULT 942
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Best Local Similarity
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RESULT 945
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Best Local
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RESULT 946

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RESULT 948

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US2003077594-A1.
                             Ouery Match
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Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
                                                                                                        Length 293;
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Novel human secreted and transmembrane protein PRO1132.
US2003203437-A1.
30-OCT-2003.
(GETH ) GENENTECH INC.
RESULT 958

ID ADC80089 standard, protein; 293 AA.
DE Novel human secreted and transmembrane protein PRO1132.
PN US_200387358-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADD41271 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003203438-A1.
                                                                                                                                                     ADD06928 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132
US2002193300-A1.
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Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
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Beet Local Similarity 45.3%; Pred. No. 1.5e-35; RESULT 963
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45.3%; Pred. No. 1.5e-35;
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Human PRO polypeptide #96.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADD53150 standard; protein; 293 AA.
Human PRO polypeptide #228.
US2003194792-A1.
                                                                                                                                                                                                                                                                                                                                                                                         ADC83175 standard; protein; 293 AA.
Human PRO polypeptide #96.
U22003059783-A1.
27-MAR-2003.
                                                                                                                                                                                                                                                                     ADD09558 standard; protein; 293 AA.
Human PRO polypeptide #228.
US2003194775-A1.
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DD ADC83175 standard; nr. DD Human PRO polver
PN US20030°
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Best Local Similarity 45.3%;
RESULT 965
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Best Local Similarity 4.

RESULT 962

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(GETH ) GENENTECH INC.
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..ry Match
Best Local Similarity
RESULT 964
ID ADD53150 stande
DE Human PRO r
PN US20031
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(GETH ) GENENTECH INC
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC
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Best Local Similarity
RESULT 960
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Best Local Similarity
RESULT 967
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Query Match 41.1%; Score 564.5; DB 7; Length 293; Best Local Similarity 45.3%; Pred. No. 1.5e-35; RESULT 976
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DB 7; Length 293;
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Novel human secreted and transmembrane protein PRO1132.
US2003087304-A1.
08-WAY-2003.
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US200220342-A1.
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41.1%; Score 564.5; DB 7; Len
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 975
ID ADE04100 standard; protein; 293 AA.
DE Human PRO polypeptide #228
PD 23-OCT-2^^-
PA '--
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Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
 41.1%; Score 564.5; DB 7
45.3%; Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
                                                                                                                                     Score 564.5; DB 7
Pred. No. 1.5e-35;
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Best Local Similarity 45.3%; Pred. No RESULT 970
DB Human PRO polypeptide #228.
PD Human PRO polypeptide #228.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADD54678 standard, protein, 293 AA.
Human PRO polypeptide #96.
US2002132253-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADD92590 standard; protein; 293 AA.
Human PRO polypeptide #228.
US2003199030-Al.
                                                                                                                                                                                    ADD02657 standard; protein; 293 AA. Human PRO polypeptide #228.
US2003203431-A1.
                                                 ADD51858 standard; protein; 293 AA. Human PRO polypeptide #228.
US2003194779-A1.
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RESULT 971
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RESULT 974
                                                                                                                                     41.1%;
45.3%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                      16-OCT-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                          30-OCT-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC
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Best Local Similarity
RESULT 972
                 Best Local Similarity RESULT 968
                                                                                                                                                 Best Local Similarity RESULT 969
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ADD80105 standard; protein; 293 AA.

Human PRO polypeptide #228.
US2003207417-A1.
06-NOV-2003.
(GETH ) GENENTECH INC.
41.1%; Score 564.5; DB 7; Length 293;
                                                        41.1%; Score 564.5; DB 7; Length 293; 45.3%; Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
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                                                                              Novel human secreted and transmembrane protein PRO1132. US2003194765-Al. 16-OCT-2003. (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADE33501 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132
US2003194767-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADE34053 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132
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Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
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Human PRO polypeptide #228.
US2003199056-A1.
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1052003194772-A1.
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Human PRO polypeptide #228.
US2003199023-A1.
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US2003199053-A1.
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45.3%;
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RESULT 981
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Best Local Similarity 45.3%;
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(GETH ) GENENTECH INC.
.ery Match
Best Local Similarity
RESULT 977
ID ADE23397 stand> DE Novel humar
PN US20031
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC
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(GETH ) GENENTECH INC
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Best Local Similarity
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                                                                                                                                                                                                 Best Local Similarity RESULT 978
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RESULT 985
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Score 564.5; DB 7; Length 293; Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
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Novel human secreted and transmembrane protein PRO1132
US2003194766-A1.
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Novel human secreted and transmembrane protein PRO1132.
US2003087305-A1.
08-MAY-2003.
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Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
Best Local Similarity 45.3%; Pred. No. 1.5e-35; RESULT 986
                                                                                                                                                                                                                                                                                      Human PRO polypeptide #228.
(0S2003199026-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human PRO polypeptide #228.
US2003203429-A1.
                                                                                                                                                                 ADE19562 standard; protein; 293 AA.
Human PRO polypeptide #228.
US2003199025-A1.
23-OCT-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                 ADE43206 standard; protein; 293 AA. Human PRO polypeptide #228. US2003199033-A1. C3-OCT-2003 (GETH ) GENENTECH INC.
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Human PRO polypeptide #228.
USZ003199064-A1.
23-OCT-2003
(GETH ) GENENTECH INC.
                                  ADD93142'standard; protein; 293 AA.
Human PRO polypeptide #228.
US2003194768-A1.
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RESULT 987
                                                                                                                                                                                                                                                   41.1%;
45.3%;
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RESULT 991
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Best Local Similarity 45.3%;
RESULT 989
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45.3%;
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Human PRO polypeptide #228.
US2003199059-A1.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                    16-OCT-2003,
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity
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Best Local Similarity
RESULT 993
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RESULT 994
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Best Local Similarity 45.3%; Pred. No. 1.5e-35; Length 293; 1D AD97582 ct. 1.5e-35; Local D AD97582 ct. 1.5e-35; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; Length 293; L
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Novel human secreted and transmembrane protein PRO1132
US2003207355-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41.1%; Score 564.5; DB 7; 45.3%; Pred. No. 1.5e-35;
                                                                                                                                                                  Score 564.5; DB 7;
Pred. No. 1.5e-35;
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Human PR01132 amino acid sequence SEQ ID NO:309.
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Pred. No. 1.5e-35;
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45.3%; Pred. No. 1.5e-35;
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Human PRO polypeptide #228.
US2003199031-A1.
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Human PRO polypeptide #228.
US2003194777-A1.
ADE42641 standard; protein; 293 AA.
Human PRO polypeptide #228.
US2003199032-A1.
23-OCT-2003.
                                                                                                                                                                                                                                                                 ADD80657 standard; protein; 293 AA.
Human PRO polypeptide #228.
US2003207418-A1.
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Human PRO polypeptide #228.
US2003199028-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADE04768 standard; protein; 293 AA.
Human PRO polypeptide #228.
US2003199034-A1.
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45.3%;
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45.3%;
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RESULT 999
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Best Local Similarity 45.3%;
RESULT 1000
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LA ) GENENTECH IN

LATY MATCH

BEST LOCAL Similarity 4

RESULT 1003

ID AD023247 standor

DE Novel humar

PN US2032°

PD 06-7
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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RESULT 1002
ID ADG21606 standard; pr.
DE Novel human secreted.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                               06-NOV-2003.
(GETH ) GENENTECH INC
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(GETH ) GENENTECH INC.
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                                                                                                                                       (GETH ) GENENTECH INC
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Novel human secreted and transmembrane protein PRO1132.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADH82019 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003207388-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADHS5938 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003207379-A1.
06-NOV-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADI64157 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003207385-A1.
06-NOV-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                          ADH55386 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003207381-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADI65106 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132
US2003207386-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 41.1%; Score 564.5; DB 7; Best Local Similarity 45.3%; Pred. No. 1.5e-35; RESULT 1008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 564.5; DB 7;
Pred. No. 1.5e-35;
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                                                                       Score 564.5; DB 7;
Pred. No. 1.5e-35;
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Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1011
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45.3%; Pred. No. 1.5e-35;
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Local Similarity 45.3%; Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
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Human PRO polypeptide #96.
US2003050457-A1.
                                                                                                                               ADG80646 standard; protein; 293 AA.
Human PRO polypeptide #228.
US2003207373-A1.
                                                                                                                                                                                                                                                                              293 AA
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RESULT 1007
                                                                         41.1%;
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ADG80094 standard, protein;
Human PRO polypeptide #228.
US2003207372-Al.
                                                                                                                                                                                                                                             45.3%;
Human PRO polypeptide #228.
US2003207370-A1.
06-NOV-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 1006
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RESULT 1010
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Best Local Similarity
RESULT 1012
                                                                                      Best Local Similarity
RESULT 1005
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(GETH ) GEN
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) 23-OCT-2003.
A (GETH ) GENENTECH INC.
Query Match 41.1%; Score 564.5; DB 8; Length 293;
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     Score 564.5; DB 8; Length 293;
Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
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                  Best Local Similarity 45.3%; Pred. RESULT 1023...
ID ADD76641 standard; protein; 293 AA. DE Human PRO polypeptide #228.
                                                                                                                                                                                                  ADD88005 standard, protein; 293 AA. Human PRO polypeptide #228. US2003092113.AL. 15-MAY.2003. (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 45.3%; Pred. RESULT 1027

ID ADE23433 standard; protein; 293 AA. BE Human PRO polypeptide #228.

PD 15-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human PRO polypeptide #228.
                                                                                                                                                                                                                                                                                                                                                  ADD86409 standard; protein; 293 AA.
Human PRO polypeptide #228.
US2003203440-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADE75857 standard; protein; 293 AA.
Human PRO polypeptide #228.
US2003211571-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADE24628 standard; protein; 293 AA.
Human PRO polypeptide #228.
US2003092111-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADE89319 standard; protein; 293 AA. Human PRO polypeptide #228. US2003199062-A1.
       41.18;
                                                                                                                                                   41.1%;
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RESULT 1025
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RESULT 1026
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Best Local Similarity 45.3%;
RESULT 1030
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(GETH ) GENENTECH INC.
                                                                                                                 29-MAY-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                                                                              Best Local Similarity RESULT 1024
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Best Local Similarity
RESULT 1029
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Best Local Similarity 45.3%; Pred. No. 1.5e-35;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
BESULT 1019
ID ADN39198 standard; protein; 293 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO.516.
PP 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
                                         Length 293;
                                                                                                                                                                      Length 293;
                                                                                                                                                                                                                                                                                                              41.1%; Score 564.5; DB 7; Length 293; 45.3%; Pred. No. 1.5e-35;
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                                                                                                                                                             Query Match
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
BESULT 1015
ID ADH81467 standard; protein; 293 AA.

DE Novel human secreted and transmembrane protein PRO1132.
PN US2003207377-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADNIGE64 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003097385-A1.
08-MAY-2003.
(GETH ) GENENTECH INC.
                                                                                        ADH99982 standard, protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132
US2003049682-A1.
13-MAR-2003.
                                                                                                                                                                                                                                                                                                                                                                                  Novel human secreted and transmembrane protein PRO1132.
US2003087355-A1.
08-MAY-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADNI6035 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003087353-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADN14931 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003087357-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADC81193 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003092115-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADN15483 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132
                                         Score 564.5; DB 7;
Pred. No. 1.5e-35;
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Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1017
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Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1018
                                                                                                                                                                                                                                                                                                                                                                       protein; 293 AA
                                     Query Match
Best Local Similarity 45.3%;
0 06-NOV-2003.
1 (GETH ) GENENTECH INC.
Query Match 4
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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RESULT 1021
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Best Local Similarity
RESULT 1022
                                                                                                                                                                                                                                                                                                                                                                     ADM82636 standard;
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ADE90646 standard; protein; 293 AA.
Human PRO polypeptide #228.
US2003199063-A1.
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                                                                                                      Score 564.5; DB 8; Length 293;
Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
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                                                                                                                                                                                                                          Length 293;
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Novel human secreted and transmembrane protein PRO1132.
US2001199051-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 564.5; DB 8;
Pred, No. 1.5e-35;
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Pred. No. 1.5e-35;
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45.3%; Pred. No. 1.5e-35;
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Pred, No. 1.5e-35;
       45.3%; Pred. No. 1.5e-35;
                        Human PRO polypeptide #228.
16-0003194794-Al.
                                                                                                                                           Human PRO polypeptide #228.
1052003199054-Al.
                                                                                                                                                                                                                                                                 ADE94787 standard; protein; 293 AA. Human PRO polypeptide #228. US2003199027-A1.
                                                                                                                                                                                                                                                                                                                                                                                        ADE91198 standard; protein; 293 AA.
Human PRO polypeptide #228.
US2003199061-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADF35435 standard; protein; 293 AA.
Human PRO1132 polypeptide.
US2003194760-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADE95339 standard; protein; 293 AA.
Human PRO polypeptide #228.
US2003199052-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADF35030 standard; protein; 293 AA.
Human PRO polypeptide #228.
US2003199029-A1.
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45.3%;
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                                                                                                        Best Local Similarity 45.3%;
RESULT 1033
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Best Local Similarity 45.3%;
RESULT 1040
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RESULT 1034
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227 Match

Best Local Similarity 4:
RESULT 1039

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DE Human PRO r.

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Best Local Similarity 4.

RESULT 1035

ID ADE91198 standa-

DE Human PRO r.

PD 23-C

PA 23-C

PA
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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                                                                               16-OCT-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Best Local Similarity
RESULT 1041
       Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Query Match 41.1%; Score 564.5; DB 8; Length 293; Best Local Similarity 45.3%; Pred. No. 1.5e-35; RESULT 1049
                                                                                                                                                                                                                                                                                                                                  Length 293;
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                                   Length 293;
                                                                                                                                                                                 Length 293;
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                                                                        ADE91793 standard; protein; 293 AA.

Novel human secreted and transmembrane protein PRO1132.
US2003199058-A1.
23-OCT-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADG24351 standard, protein, 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003207426-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADG22158 standard, protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003207360-A1.
                                                                                                                                                                                                                                                                                                        Best Local Similarity 45.3%; Pred. No. 1.5e-35; RESULT 1044

ID ADG02372 standard; protein; 293 AA.

DE Human PRO polypeptide #228.

PD 06-NOV-2003.

PA (GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.

ery Match
41.1%; Score 564.5; DB 8;

ery Match
45.3%; Pred. No. 1.5e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 41.1%; Score 564.5; DB 8;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1046
                                   DB 8;
                                                                                                                                                                                                                                                                                                                                    DB 8;
                                                                                                                                                                                 Score 564.5; DB 8;
Pred. No. 1.5e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match .41.1%; Score 564.5; DB 8
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
                                   Query Match 41.1%; Score 564.5; DB 8
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
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US2003208055-Al.
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US2003207422-A1.
                                                                                                                                                                                                                                        ADG11685 standard; protein; 293 AA.
Human PRO1132 polypeptide.
US2003228655-A1.
11-DEC-2003.
(GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 45.3%; P1
RESULT 1048
ID ADG24351 standard; protein; 293
DE Novel human secreted and transm PN W32003207426-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41.1%;
                                                                                                                                                                                 Query Match 41.1%;
Best Local Similarity 45.3%;
RESULT 1043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADG20228 standard; protein;
Human PRO polypeptide #228.
US2003207376-A1.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
23-OCT-2003.
(GETH ) GENENTECH INC.
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(GETH ) GEN
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Best Local Similarity 45.3%; Score 564.5; DB 8; Length 293; BEST Local Similarity 45.3%; Pred. No. 1.5e-35; ID ADG15632 standard; protein; 293 AA. DE Human PRO polypeptide #228. PN US203219885-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vuery Match
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RRSULT 1054
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PA (GETH ) GENENTECH INC.

Query Match 41.1%; Score 564.5; DB 8; Length 293;

Best Local Similarity 45.3%; Pred. No. 1.5e-35;

RESULT 1056
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Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1058
                                                                                       41.1%; Score 564.5; DB 8; Length 293; 45.3%; Pred. No. 1.5e-35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 293;
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Pred. No. 1.5e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADG08462 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132
US2003207424-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 41.1%; Score 564.5; DB 8; Best Local Similarity 45.3%; Pred. No. 1.5e-35; RESULT 1053
ID ADG05201 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207375-A1.
                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 45.3%; Pred. No
RESULT 1052.

ID ADG1684 standard; protein; 293 AA.
DE Human PRO polypeptide #228.
PN US2003207359.Al.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
                                                                                                                                              MDF92257 standard; protein; 293 AA.
Human PRO polypeptide #228.
US2003207353-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADG19568 standard; protein; 293 AA.
Human PRO polypeptide #228.
US2003207425-A1.
06-NOV-2003.
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Human PRO polypeptide #228.
US2003207357-A1.
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US2003207371-A1.
06-NOV-2003.
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Human PRO polypeptide #228.
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Local Similarity 45.3%;
Human PRO polypeptide #228
US2003207351-A1.
06-NOV-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Query Match
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(GETH ) GENENTECH INC.
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                                                                                    Query Match
Best Local Similarity
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Query Match

41.1%; Score 564.5; DB 8; Length 293;

Best Local Similarity 45.3%; Pred. No. 1.5e-35;

ID ADG60997 standard; protein; 293 AA.

DE Novel human secreted and transmembrane protein PRO1132.

PN US2003207390-A1.
                                                                                                                                                                                            vuery Match 41.1%; Score 564.5; DB 8; Length 293;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1061
                                                                                                                                                                                                                                                                           Score 564.5; DB 8; Length 293; Pred. No. 1.5e-35;
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Best Local Similarity 45.3%; Pred. No. 1.5e-35;
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Best Local Similarity 45.3%; Pred. No. 1.5e-35; RESULT 1060, D. ADG23799 standard; protein; 293 AA. DE Novel human secreted and transmembrane protein PRO1132. P. Oc-NOV-2003.

A (GETH ) GENENTECH INC.
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Novel human secreted and transmembrane protein PRO1132.

1 US2003194778-A1.

1 16-OCT - 2003.

1 (GETH ) GENENTECH INC.

41.1%; Score 564.5; DB 8; Lengt
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Novel human secreted and transmembrane protein PRO1132.
US2003207427-A1.
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Novel human secreted and transmembrane protein PRO1132.
US2003207350-A1.
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Novel human secreted and transmembrane protein PRO1132.
US2003207356-A1.
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Novel human secreted and transmembrane protein PRO1132.
US2003207428-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vuery Match
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 41.1%; Score 564.5; DB 8; Best Local Similarity 45.3%; Pred. No. 1.5e-35; RESULT 1064
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Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 41.1%; Score 564.5; DB 8
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1063
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Human PRO polypeptide #228.
US2003207358-A1.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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41.1%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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Query Match
Best Local Similarity
RESULT 1078
ID ADH19555 standard; pr
DE Human secreted/transm
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH ) GENENTECH INC
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Query Match
Best Local Similarity
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RESULT 1081
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 564.5; DB 8; Length 293;
Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
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                                        Score 564.5; DB 8; Length 293;
Pred. No. 1.5e-35;
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Novel human secreted and transmembrane protein PRO1132.
US2003207420-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADG56093 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003207363-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADG53677 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003207415-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADG71563 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132 US2003207421-A1.
                                                                             ארטייים אלא 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003207362-A1.
                                                                                                                                                                                                                               ADG56989 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003207364-A1.
                                                                                                                                                                                                                                                                                                                                                                               ADG55885 standard, protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003207365-A1.
06-NOV-2003.
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Novel human secreted and transmembrane protein PRO1132
US2003207368-A1.
                                                                                                                                                                                                                                                                                                                           41.1%; Score 564.5; DB 8; 45.3%; Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
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Human PRO polypeptide #228.
US2003207805-A1.
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Best Local Similarity 45.3%;
RESULT 1075
                                                                                                                                                                                   41.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41.18;
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Local Similarity 45.38;
                                          Query Match 41.1%;
Best Local Similarity 45.3%;
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC
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(GETH ) GENENTECH INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GETH ) GENENTECH INC
                                                                                                                                                                                                Best Local Similarity
RESULT 1070
                                                                                                                                                                                                                                                                                                                                          Best Local Similarity RESULT 1071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity RESULT 1072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best_Local Similarity RESULT 1076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
RESULT 1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-NOV-2003
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Score 564.5; DB 8; Length 293; Pred. No. 1.5e-35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 293;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 293;
Score 564.5; DB 8; Length 293; Pred. No. 1.5e-35;
                                                                                                                                                       Length 293;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AD556437 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003207366-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADH12703 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003207378-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Auco4229 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
                                                                                                                                                                                                                                                                                                                                           AUM12079 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADG52501 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003207414-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 41.1%; Score 564.5; DB 8;
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1085
                                                                                                                                                     Score 564.5; DB 8;
Pred. No. 1.5e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      41.1%; Score 564.5; DB 8; 45.3%; Pred. No. 1.5e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 564.5; DB 8;
Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
                                                                                                                                                                                                                                                                                                         DB 8;
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Pred. No. 1.5e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 41.1%; Score 564.5; DB 8
Best Local Similarity 45.3%; Pred. No. 1.5e-35;
RESULT 1082
                                                                                                                                                                                                                                                                                                         41.1%; Score 564.5; DB 8
45.3%; Pred. No. 1.5e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADH21048 standard; protein; 293 AA.
Human secreted/transmembrane protein PRO1132.
US2003224358-A1.
                                                        ADH19555 standard; protein; 293 AA. Human secreted/transmembrane protein PRO1132. US2003228656-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human PRO polypeptide #228. US2003194793-A1.
                                                                                                                                                                                                           ADH30712 standard; protein; 293 AA.
Human PRO polypeptide #228.
US2003077723-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USZUGAT.
16-0CT-2003.
(GETH ) GENENTECH INC.
*** MATCh '''rity 45.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 45.3%;
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                                                                                                              PD 11-DEC-2003.

PA (GETH ) GENENTECH INC.

QUELY MARCh 41.1%;

Best Local Similarity 45.3%;

RESULT 1079
                                                                                                                                                                                                                                                                                                                Best Local Similarity 45.3%; RESULT 1080
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RESULT 1087

ID ADG6154

DE Novel hi
PN US20032

PD 06-NOV-PA (GETH)

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ADI14791 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132
US2003207383-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADJ65684 standard; protein; 293 AA.
Human PRO polypeptide #228.
US2004038335-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein; 293 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADM28406 standard; protein; 293 AA.
Human PRO polypeptide #228.
US2004077064-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein; 293 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       293 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MOUN ) MOUNT SINAI HOSPITAL. (YOUS/) YOUSEF G.
                                                                                                                                                                                                                41.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41.1%;
45.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41.1%;
                                                                             Query Match 41.1%;
Best Local Similarity 45.3%;
RESULT 1097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 41.1%;
Best Local Similarity 45.3%;
RESULT 1101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human kallikrein 5 protein.
WO2004021008-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 45.3%;
RESULT 1104
                                                                                                                                                                                                                                                                                                                                                                                                                  Human PRO polypeptide #228
US2004038336-A1.
26-FEB-2004.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human PRO polypeptide #228
US2004058424-A1.
                                                06-NOV-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                 06-NOV-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                 26-FEB-2004.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-APR-2004.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-FEB-2004.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                              Best Local Similarity
RESULT 1098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
RESULT 1105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity RESULT 1100
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ID ADK52481 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
RESULT 1103
                                                                                                                                                                                                                                                                                                                                                                                                  ADJ77562 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADM42544 standard;
                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                   DB 8; Length 293;
                                                                                              Length 293;
                                                                                                                                                                                                                                                                                                                                                                 Score 564.5; DB 8; Length 293;
Pred. No. 1.5e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 8; Length 293;
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Pred. No. 1.5e-35;
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             ADG61549 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003207429-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADG09336 standard, protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
15-2004009547-A1.
15-3AN-2004.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                ADG54781 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003207367-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADG59821 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2003207369-A1.
06-NOV-2003.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADG09988 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132
US2004009548-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADI15459 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132
                                                                                              Score 564.5; DB 8;
Pred. No. 1.5e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 564.5; DB 8 Pred. No. 1.5e-35;
                                                                                                                                                                                                                                  Score 564.5; DB B Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 564.5; DB 8 Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
                                                                                                                                             ADH20088 standard; protein; 293 AA.
Human secreted/transmembrane protein PRO1132.
US2003219856-A1.
                                                                                                                                                                                                                                                                               ADH28636 standard; protein; 293 AA.
Human PRO polypeptide #228.
US2003022331-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADIB1245 standard; protein; 293 AA
Human PRO polypeptide #228.
US2003207361-A1.
                                                                                                                                                                                                                                41.18;
45.38;
                                                                                              41.1%;
                                                                                                                                                                                                                                                                                                                                                                 41.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 41.1%;
Best Local Similarity 45.3%;
RESULT 1095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JAN-2004.
(GETH ) GENENTECH INC.
                                       J-J.

2003.

AH ) GENENTECH I.

LY MATCh

BEST LOCAL SIMILARITY A

RESULT 1088

ID ADH20088 stands

DE Human secre

PN US20031
                                                              06-NOV-2003.
(GETH ) GENENTECH INC.
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(GETH ) GENENTECH INC.
                                                                                                                                                                                                               (GETH ) GENENTECH INC
Query Match
                                                                                                                                                                                                                                                                                                                                                  (GETH ) GENENTECH INC
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(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GETH ) GENENTECH INC
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                                                                                                                                                                                                                                            Best Local Similarity RESULT 1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
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Best Local Similarity
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Query Match

Query Match

Best Loca RESULT 1091

Query Match

Query Match

RESULT 1094

Query Match

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Length 293;
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                                                                                                                                                   Length 293;
                                                                                                                                                                                                                                                                                                'Match 41.1%; Score 564.5; DB 8; Length 293; Local Similarity 45.3%; Pred. No. 1.5e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 564.5; DB 8; Length 293;
Pred. No. 1.5e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 293;
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                                        Novel human secreted and transmembrane protein PRO1132.
                                                                                                                                                                                                   ADJ6567 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132.
US2004039164-A1.
Score 564.5; DB 8;
Pred. No. 1.5e-35;
                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 564.5; DB 8;
Pred. No. 1.5e-35;
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Pred. No. 1.5e-35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41.1%; Score 564.5; DB 8 45.3%; Pred. No. 1.5e-35;
                                                                                                                                                 Score 564.5; DB 8
Pred. No. 1.5e-35;
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Ovarian cancer-associated protein #46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human ovarian cancer-related tumour marker kallikrein 5 (hK5) protein. WO2004075713-A2. 10-SEP-2004. (MOUN ) MOUNT SINAI HOSPITAL.
                                                                                                                                                                                                                                                                                                                           RESULT 1107

ID ADR72621 standard; protein; 293 AA.

ID ADR72621 standard; protein; 293 AA.

DE Human renal cell carcinoma-related kallikrein 5 (hK5) protein.

PN WO200407006-A2.

PD 10-SEP-2004.

PD 10-SEP-2004.

A1 1%: Score 564.5; DB 8; Length 293;
                                                                                                           41.1%; Score 564.5; DB 8; Length 293; 45.3%; Pred. No. 1.5e-35;
                                                                                                                                                                                                                                                                                    Ouery Match 41.1%; Score 564.5; DB 8; Length 293; Best Local Similarity 45.3%; Pred. No. 1.5e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41.1%; Score 564.5; DB 2; Length 322; 45.3%; Pred. No. 1.6e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              41.1%; Score 564.5; DB 8; Length 293; 45.3%; Pred. No. 1.5e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41.1%; Score 564.5; DB 8; Length 293, 45.3%; Pred. No. 1.5e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 564; DB 2; Length 276; Pred. No. 1.5e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41.0%; Score 564; DB 3; Length 276; 45.9%; Pred. No. 1.5e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41.0%; Score 564; DB 5; Length 276; 45.9%; Pred. No. 1.5e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 276;
                                                                                                                                                                         ADI96440 standard; protein; 293 AA.
Novel human secreted and transmembrane protein PRO1132
US2003207354-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 1113

ID AAU82729 standard; protein; 276 AA.

DE Amino acid sequence of novel human protease #28.

PN WC20200860-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-DEC-1996.
(NEWE-) NEW ENGLAND MEDICAL CENT HOSPITALS INC.
Query Match 41.0%; Score 564; DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABG96356 standard; protein; 276 AA.
Human ovarian cancer marker OV32.
W020021928-A2.
19-SEP-2002.
(MILL-) MILLENNIUM PHARM INC.
ETY MATCH 41.0%; Score 564; DB 5; St. Local Similarity 45.9%; Pred. No. 1.5e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 1110
ID AAW07620 standard; protein; 276 AA.
DE Human NESI polypeptide.
PN W09639175-A1.
AD195888 standard; protein; 293 AA.
Human PRO polypeptide #228.
US2003077659-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY14072 standard; protein; 322 AA.
Human BS247 specific epitope.
WO9922027-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADR72873 standard; protein; 293 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB21327 standard; protein; 276 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADB80527 standard; protein; 276 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N WO200053776-A2.
14-SRP-2000.
(MOUN ) MOUNT SINAI HOSPITAL.
QUELY MATCH 41.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41.0%;
45.9%;
                                                                                                                                                                                                                                           06-NOV-2003.
(GETH ) GENENTECH INC.
                                                                24-APR-2003.
(GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
RESULT 1109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity RESULT 1108
                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity RESULT 1111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity RESULT 1114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-MAY-1999.
(ABBO ) ABBOTT LAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-JAN-2002.
(SUGE-) SUGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human NESI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                         RESULT 1106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 1112
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ADR72886 standard; protein; 276 AA.
ADR72886 standard; protein; 276 AA.
Wowno vovarian cancer-related tumour marker kallikrein 10 (hK10) protein.
WO2004075713-A2.
10-SEP-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PN WOLVEY.

PN WOLVEY.

PN 05-406-2004.

PA (MILL-) MILLENNIUM PHARM INC.

Query Match

Best Local Similarity 45.9%; Pred. No. 1.5e-35;

RESULT 1119

ID ADR72628 standard; protein; 276 AA.

DE Human renal cell carcinoma-related kallikrein 10 (hK10) protein.

PN WOLOGO4077060-A2.

PD 10-SEP-2004.

PA (MOUN ) MOUNT SINAI HOSPITAL.

PA (MOUN ) MOUNT SINAI HOSPITAL.

Query Match

41.0%; Score 564; DB 8; Length 276;
                                                                                                                                                                                                                                                                                                                                                                    ADN39880 standard; protein; 276 AA.
Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C250.
WO2003042661-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PD 14-SEP-2000.

PA (MODN) MOUNT SINAI HOSPITAL.

Query Match

40.9%; Score 562; DB 3; Length 237;

Best Local Similarity 48.1%; Pred. No. 1.9e-35;

RESULT 1122

ID AAB21299 standard; protein, 256 AA.

DE AMB21299 standard; protein #1.

PN WO200053776-A2.

PD 14-SEP-2000.

PA (MOUN ) MOUNT SINAI HOSPITAL.

QUERY MAtch

Best Local Similarity 49.1%; Pred. No. 2.2e-35;

Best Local Similarity 49.1%; Pred. No. 2.2e-35;
                                           Query Match 41.0%; Score 564; DB 7; Length 276; Best Local Similarity 45.9%; Pred. No. 1.5e-35; RESULT 1115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 41.0%; Score 564; DB 7; Length 276; Best Local Similarity 45.9%; Pred. No. 1.5e-35; RESULT 1117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MOUN) MOUNT SINAI HOSPITAL.

ry Match
t Local Similarity 45.9%; Pred. No. 1.5e-35;
                                                                                                                                                                                                                                                                                        Length 276;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADQ89070 standard; protein; 276 AA.
Human urological disorder related protein 2045 SEQ:22.
WO2004065576-A2.
                                                                                                                                                                                                                                                       PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 45.9%; Pred. No. 1.5e-35;
RESULT 1116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vuery Match
Best Local Similarity 45.9%; Pred. No. 1.5e-35;
RESULT 1118
                                                                                                                                                        ADE40473 standard; protein; 276 AA.
Human kallikrein 10 (gene ID 2045) protein.
WO2003070883-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADN04446 standard; protein; 276 AA. Antipsoriatic protein sequence #416. WO2004028479-A2. GB-APR-2004. (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB21305 standard; protein; 237 AA. Human KLK-L6 protein #1. WO200053776-A2.
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Human KLK-L2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                22-MAY-2003.
(EOSB-) EOS BIOTECHNOLOGY INC.
WO2002102235-A2.
27-DEC-2002.
(EOSB-) EOS BIOTECHNOLOGY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
RESULT 1121
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Query Match
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Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:530.
           (MOUN) MOUNT SINAI HOSPITAL, (MOUN) MOUNT SINAI HOSPITAL, ery Match 40.9%; Score 561.5; DB 3; Length 287; ery Match 46.1%; Pred. No. 2.5e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ID ADB80567 standard; protein; 244 AA.

ID ADS80567 standard; protein; 244 AA.

IDE Ovarian cancer-associated protein #66.

PN WO2002102235-A2.

PA (EOSB-) EOS BIOTECHNOLOGY INC.

Query Match

40.8%; Score 561; DB 7; Length 244;

Best Local Similarity 46.7%; Pred. No. 2.3e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAMSI006 standard; protein; 244 AA.

Protease M, a novel serine protease.

N W09811238-A2.

19-MAR-1998.

Ouery Match

Query Match

Best Local Similarity 46.7%; Pred. No. 2.3e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         y Match 40.8%; Score 561; DB 6; Length 244; Local Similarity 46.7%; Pred. No. 2.3e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 40.8%; Score 561; DB 2; Length 244; Best Local Similarity 46.7%; Pred. No. 2.3e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40.8%; Score 561; DB 2; Length 244; 46.7%; Pred. No. 2.3e-35;
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                                                                                                                                                                                                                                                           Length 228;
                                                                                                                                                                                                                                                                                                                                                                                                                              Length 239;
                                                                                                          DE Synthetic shortened trypsinogen SEQ ID NO 23.

PN WO200261064-A2.

PD 08-AUG-2002.

PA (HOFF) ROCHE DIAGNOSTICS GMBH.

PA (HOFF) HOFFMANN LA ROCHE & CO AG F.

Query Match

Rest Local Similarity 46.7%; Pred. No. 2.1e-35;

RESULT 1125
                                                                                                                                                                                                                                                                                                                                DE Human zyme.
PN W0200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 40.8%; Score 561; DB 3;
Best Local Similarity 46.7%; Pred. No. 2.3e-35;
RESULT 1126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40.8%; Score 561; DB 3; 46.7%; Pred. No. 2.3e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR44532 standard; protein; 244 AA.
Zyme APP-cleaving protease.
BP576152-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW22985 standard; protein; 244 AA.
Human serine protease 59 (SP59).
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                                                                                                                                                                                                                                                                                                                   AAB21310 standard; protein; 239 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-SBP-2000.
(MOUN ) MOUNT SINAI HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-MAY-2003.
(MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-DEC-1993.
(ELIL ) LILLY & CO ELI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N JP09149790-A.
1 10-JUN-1997.
A (SUNR ) SUNTORY LTD.
Query Match
                                                         Query Match
Best Local Similarity
RESULT 1124
ID ABB98259 standard; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity RESULT 1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity RESULT 1129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human zyme.
WO200053776-A2.
WO200053776-A2.
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RESULT 1131
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ADR72876 standard; protein; 244 AA.
Human ovarian cancer-related tumour marker kallikrein 6 (hK6) protein.
MO2004075713-A2.
(MOUN ) MOUNT SINAI HOSPITAL.
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Human renal cell carcinoma-related kallikrein 6 (hK6) protein.
WO2004077060-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR67888 standard; protein; 253 AA.
Human stratum corneum chymotrophic recombinant enzyme (SCCE)
WO9500651-A1.
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 40.8%; Score 561; DB 8; Length 244; Best Local Similarity 46.7%; Pred. No. 2.3e-35; RESULT 1134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 40.8%; Score 561; DB 8; Length 244; Best Local Similarity 46.7%; Pred. No. 2.3e-35; RESULT 1135
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Query Match
40.8%; Score 560; DB 5; Length 244;
Best Local Similarity 46.9%; Pred. No. 2.7e-35;
                                                                                       Length 244;
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Best Local Similarity 44.6%; Pred. No. 6.9e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADQ89076 standard; protein; 244 AA.
Human urological disorder related protein 2047 SEQ:28.
WO2004065576-A2.
                                                                                   Ouery Match 40.8%; Score 561; DB 7;
Best Local Similarity 46.7%; Pred. No. 2.3e-35;
RESULT 1133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PD 10-SEP-2004.
PA (MOUN ) MOUNT SINAI HOSPITAL.
Query Match 40.8%; Score 561; DB 8;
Best Local Similarity 46.7%; Pred. No. 2.3e-35;
RESULT 1137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PD 05-40G-2004.

PA (MILL-) MILLENNIUM PHARM INC.

Query Match 40.8%; Score 561; DB 8;

Best Local Similarity 46.7%; Pred. No. 2.3e-35;

RESULT 1136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WOLOUSE
14-SEP-2000.
(MOUN) MOUNT SINAI HOSPITAL.
Hery Match
A0.5%; Score 557; DB 3;
A0.1%; Pred. No. 5.7e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW05383 standard; protein; 253 AA.
Human amyloid precursor protein protease.
WO9631122-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADN29289 standard; protein; 244 AA.
Human kallikrein 6 associated protein.
US204097452-Al.
20-MAY-2004.
(ISIS-) ISIS PHARM INC.
                                                                                                                                                                                                               ADNO4074 standard; protein; 244 AA. Antipsoriatic protein sequence #232. WO2004028479-A2. GB-APR-2004. (GETH ) GENENTECH INC.
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Human ovarian cancer marker OV33.
WQ200211928-A2.
19-SEP-2002.
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(EOSB-) EOS BIOTECHNOLOGY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JAN-1995.
(SYMB-) SYMBICOM AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
RESULT 1139
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Best Local Similarity
RESULT 1140
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Best Local Similarity
RESULT 1155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US2004038223-A1.
26-FEB-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GUO X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human NOV18b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AGEE/)
(BERG/)
(DIPI/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MILL/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PENA/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (KEKU/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANDE/
ZHON/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ELLE/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GORM/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STON/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ROTH/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Gnox/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MALY/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RAST/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JIWW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABRE88471 standard; protein; 253 AA.
Human stratum corneum chymotryptic enzyme - ovarian cancer clone O1676P.
WO2003029468-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADJ68833 standard; protein; 253 AA.
Human heat mitochondrial protein as a therapeutic target SeqID639.
WO2003087768-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABU07471 standard; protein; 253 AA.
Protein differentially regulated in prostate cancer #74.
W0200281638-A2.
17-0CT-2002.
17-0CT-2002.
CORIG-) ORIGENE TECHNOLOGIES INC.
ery Match
st Local Similarity 44.6%; Pred. No. 6.9e-35;
                                 Length 253;
                                                                                                                                                                                              40.4%; Score 555; DB 5; Length 253; 44.6%; Pred. No. 6.9e-35;
                                                                                                                                                                                                                                                                                                                                                          Score 555; DB 5; Length 253; Pred. No. 6.9e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40.4%; Score 555; DB 5; Length 253; 44.6%; Pred. No. 6.9e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 555; DB 7; Length 253;
Pred. No. 6.9e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABU07440 standard; protein; 253 AA. Protein differentially regulated in prostate cancer #43. WO200281638-A2.
                                                                                    peptide; 253 AA.
N-terminal fragment SEQ ID 48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WALCOLOGO.
27-DEC-2002.
(EOSB-) EOS BIOTECHNOLOGY INC.
(EOSB-) EOS BIOTECHNOLOGY INC.
40.4%; Score 555; DB 7;
Lery Match
1 c'milarity 44.6%; Pred. No. 6.9e-35;
                                                                                                                                                                                                                                                                                                                                                                                                               AAMB2740 standard; protein; 253 AA.
Amino acid sequence of novel human protease #39,
W0200200860-A2.
(3-JAN-2002.
(SUGE-) SUGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40.4%; Score 555; DB 6; 44.6%; Pred. No. 6.9e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-OCT-2002.

(ORIG-) ORIGENE TECHNOLOGIES INC.

Query March
40.4%; Score 555; DB 6;

Best Local Similarity 44.6%; Pred. No. 6.9e-35;
                                   Score 555; DB 2;
Pred. No. 6.9e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADB80484 standard; protein; 253 AA.
Ovarian cancer-associated protein #24.
WO2002102235-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 44.6%; Pred. RESULT 1150
ID ADN39180 standard; protein; 253 AA.
                                                                                                                                                                                                                                                       ABB84406 standard; protein; 253 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40.48;
44.68;
                                                                                                                                                                                                                                                                                                                                                              40.4%;
                            Query Match
Beet Local Similarity 44.6%;
RESULT 1142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-OCT-2003.
(MITO-) MITOKOR.
(BUCK-) BUCK INST AGE RES.
10-OCT-1996.
(ELIL ) LILLY & CO ELI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CORI-) CORIXA CORP.
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity RESULT 1149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity RESULT 1145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
RESULT 1147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
RESULT 1148
                                                                                                                                                                                              Query Match
Best Local Similarity
RESULT 1143
                                                                                                                                                                                                                                                                         Human SCCE protein.
WO200262135-A2.
15-AUG-2002.
                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
RESULT 1144
                                                                                      ABB84421 standard;
Human SCCE protein
WO200262135-A2.
                                                                                                                                             15-AUG-2002.
(EGEL/) EGELRUD T.
(HANS/) HANSSON L.
                                                                                                                                                                                                                                                                                                                            (EGEL/) EGELRUD T. (HANS/) HANSSON L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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RESULT 1152

ID ADNO4182 standard; protein; 253 AA.

DB Antipsoriatic protein sequence #286.

DB Antipsoriatic protein sequence #286.

PN WOLO4028479-A2.

PN WOLO4028479-A2.

PD 08-ARR-2004.

Query Match

Best Local Similarity 44.6%; Pred. No. 6.9e-35;

RESULT 1153

DE Human ovarian cancer-related tumour marker kallikrein 7 (hK7) protein.

PN WOLO604075713-A2.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:498.
PN W02003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 40.4%; Score 555; DB 7; Length 253;
Best Local Similarity 44.6%; Pred. No. 6.9e-35;
                                                                                                                                                                   ADLO6515 standard; protein; 253 AA.

Human tumour-associated antigenic target (TAT) polypeptide #14.

WO2004016225-A2.
26-FEB-2004.

(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40.3%; Score 553.5; DB 6; Length 252; 46.6%; Pred. No. 9e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PD 10-SEP-2004.

PA (MOUN) MOUNT SINAI HOSPITAL.

Query Match 40.4%; Score 555; DB 8; Length 253;

Best Local Similarity 44.6%; Pred. No. 6.9e-35;

RESULT 1154
                                                                                                                                                                                                                                                                            Length 253;
                                                                                                                                                                                                                                                                          Query Match 40.4%; Score 555; DB 8;
Best Local Similarity 44.6%; Pred. No. 6.9e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADA05734 standard; protein; 252 AA.
Human NOV18b protein SEQ ID NO:94.
WO2003029424-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADN62898 standard; protein; 252 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STONE D J.
PENA C E A.
SHENOY S G.
SHIMKETS R A.
ROTHENBERG M E.
LEACH M D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPYTEK K A.
BDINGER S R.
ELLERMAN K.
MALYANKAR U M.
ORT T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GORMAN L.
ZERHUSEN B D.
ANDERSON D W.
ZHONG M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-APR-2003.
(CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PATTURAJAN M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGEE M L.
BERGHS C.
DIPIPPO V A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MILLET I.
PEYMAN J A.
KEKUDA R.
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Recombinant trypsin.
WO200017332-A1.
30-MAR+2000.
(ELIL ) LILLY & CO ELI.
                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity RESULT 1164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
RESULT 1166
                                                                                                                                                                                                                                                                                                                           15-AUG-2002.
(EGEL/) EGELRUD T.
(HANS/) HANSSON L.
                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                   ID AAY08025 standard; protein; 253 AA.

DE Mouse protease-related protein (PVP).

PD 24-DEC-1998.

PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

QUETY MATCh

Best Local Similarity 43.5%; Pred. No. 9e-35;

RESULT 1157
                                       vuery match
Best Local Similarity 46.6%; Pred. No. 9e-35;
RESULT 1156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 44.8%; Score 553; DB 8; Length 250;
RESULT 1158
ID AAA777494 standard; protein; 229 AA.
DE Bovine trypsingen.
PN WO200005384-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 40.2%; Score 552; DB 2; Length 230; Beet Local Similarity 47.5%; Pred. No. 1.1e-34; RESULT 1160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vuery Match 40.2%; Score 552; DB 3; Length 229;
Best Local Similarity 46.3%; Pred. No. 1.1e-34;
RESULT 1159
                                                                                                                                                                                      ADN62896 standard; protein; 250 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR53638 standard; protein; 230 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY91926 standard; protein; 231 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SASTY) KASIBELL STONN) STONE D. J. PENA, PENA C B A. SHEN, SHENOY S G. (SHIM), SHIRKETS R A. (ROTH), ROTHENBERG M E. (LEAC,) LEACH M D. (AGEE), BERGHS C. (DIPI) DIFIPPO V A. (BISE,) BISEN A. (GANG), GANGOLLI E A. (RIEG), RIBGER D K. (RIEG), RIBGER D K. (RIEG), RIBGER D K. (RIEG), RIBGER D K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-MAY-1994.
(ELIL ) LILLY & CO ELI.
                                                                                                                                                                                                                                                                                                            GUO X.
PATTURAJAN M.
SPYTEK K A.
DINGER S.
BLIEBNAN K.
(EISE/) EISEN A.
(GANG/) GANGOLLI E A.
(RIEG/) RIEGER D K.
(SPAD/) SPADERNA S K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (PROD-) PRODIGENE INC.
                                                                                                                                                                                                                                                                                                                                                                                                               ZERHUSEN B D. ANDERSON D W.
                                                                                                                                                                                                                                                  MILLET I.
PEYMAN J A.
KEKUDA R.
                                                                                                                                                                                                                                                                                                                                                                                                                                       ZHONG M.
CATTERTON E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MILLER C E.
RASTELLI L.
                                                                                                                                                                                                                                       SMITHSON G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bovine trypsinogen.
EP597681-A1.
                                                                                                                                                                                                                                                                                                                                                                                        ORT T.
GORMAN L.
                                                                                                                                                                                                              US2004038223-A1.
                                                                                                                                                                                                    Human NOV18a
                                                                                                                                                                                                                                                                                                                                      (SPYT/)
(EDIN/)
(ELLE/)
(MALY/)
                                                                                                                                                                                                                                                                                                                                                                                                                            ANDE/)
                                                                                                                                                                                                                                                                                     (LILL/)
(GUOX/)
                                                                                                                                                                                                                                                                                                                                                                                      (ORTT/)
(GORM/)
(ZERH/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RAST/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (/MMID
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DE Connective tissue antigen (CTA) #243.

DE Connective tissue antigen (CTA) #243.

PN US2003054375-A1.

PD 20-MAR-2003.

Query Match 39.8%; Score 547.5; DB 7; Length 247;

Best Local Similarity 46.1%; Pred. No. 2.6e-34;

RESULT 1169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel human connective tissue related polypeptide #243.
Novel human connective tissue related polypeptide #243.
W020155433-A1.
02-AUG-2001.
(HUMA-) HUMAN GENOME SCI INC.
ery Match
st Local Similarity 46.1%; Pred. No. 2.6e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 39.8%; Score 547.5; DB 4; Length 247;

Best Local Similarity 46.1%; Pred. No. 2.6e-34;

RESULT 1167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 39.8%; Score 547.5; DB 4; Length 247;
Best Local Similarity 46.1%; Pred. No. 2.6e-34;
RESULT 1168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 3; Length 247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40.1%; Score 550.5; DB 5; Length 249; 46.7%; Pred. No. 1.5e-34;
Query Match .40.2%; Score 552; DB 3; Length 231; Best Local Similarity 46.3%; Pred. No. 1.1e-34; RESULT 1161
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 250;
                                                                                                                                                                                                                                        Length 231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB84420 standard; peptide; 249 AA.
Porcine SCCE protein N-terminal fragment SEQ ID 47.
WO200262135-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ID AAB35701 standard; protein; 247 AA.

ID AAB35701 standard; protein; 247 AA.

EN Human trypsin hL amino acid sequence.

PN J9-SEP-2000.

PA (TTPH-) TT PHARMA KK.

Query Match 40.0%; Score 549.5; DB 3;

Best Local Similarity 44.0%; Pred. No. 1.8e-34;

RESULT 1165
                                                                                                                                                                                                                                                                                                                                                                                   PD 10-APR-2003.

PA (CURA-) CURAGEN CORP.

Query Match

Best Local Similarity 44.8%; Pred. No. 1.2e-34;

RESULT 1163
                                                                                                                            DE Bovine met-phe-trypsinogen.
PN W0200119970-A2.
PD 22-MR-2001.
PA (ELIL) LILLY & CO ELI.
Query Match
Bost Local Similarity 46.3%; Pred. No. 1.1e-34;
RESULT 1160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU17043 standard; protein; 247 AA.
Human novel secreted protein, SEQ ID 284.
WO200155441-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU23752 standard; protein; 247 AA. Novel human enzyme polypeptide #838 WO200155301-A2.
                                                                                                                                                                                                                                                                                                                   ADA05732 standard; protein; 250 AA.
Human NOV18a protein SEQ ID NO:92.
WO2003029424-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW81767 standard; peptide; 223 AA
                                                                                                      AAB80953 standard; protein; 231 AA
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Best Local Similarity RESULT 1183
                                                                                                                                                                                                                                                                                                                                                                               SMITHSON G.
MILLET I.
PEYMAN J A.
KEKUDA R.
                                                                                                                                                                                                                                                                                                                          Human NOV18f.
US2004038223-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GUO X.
                                                                                                                                                                                                                                                                                                                                                               26-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                     (/LIWS)
                                                                                                                                                                                                                                                                                                                                                                                                                                            KEKU/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (AGEE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (LEAC/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BERG/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (/IdId)
                                                                                                                                                                                                                                                                                                                                                                                                                        (PEYM/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (STON/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /NOHZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (حوود)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MALY/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GORM/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZERH/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ROTH/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SPYT/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (JIWW/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RAST/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SHEN/
                                                                                                                                                                                                                                                                 LT 1171
ABG31841 standard; protein; 223 AA.
ABG31841 standard; protein; 223 AA.
ABG31841 standard; protein; 223 AA.
BXample protein #3 used in three-dimensional structure analysis method.
WO200287954-A1.
25-JUL-2002.
(MITU ) MITSUBISHI CHEM CORP.
(UMEY/) UMEYAMA H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 39.8%; Score 547; DB 2; Length 224; Best Local Similarity 46.1%; Pred. No. 2.5e-34; RESULT 1175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 39.8%; Score 547; DB 3; Length 233; Best Local Similarity 46.1%; Pred. No. 2.6e-34; RESULT 1176
                                                                            Length 223;
                                                                                                                                                                                          02-DEC-1999.
(MEDI-) INST MEDICINAL MOLECULAR DESIGN INC.
39.8%; Score 547; DB 3; Length 223; st Local Similarity 46.1%; Pred. No. 2.5e-34;
                                                                                                                                                                                                                                                                                                                                                                                                    39.8%; Score 547; DB 5; Length 223; 46.1%; Pred. No. 2.5e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39.8%; Score 547; DB 7; Length 223; 46.1%; Pred. No. 2.5e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 546; DB 8; Length 244; Pred. No. 3.3e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 223;
                                     27-OCT-1998.
(IYAK-) IYAKU BUNSHI SEKKEI KENKYUSHO KK.
ery Match
19.8%; Score 547; DB 2;
ery Match 46.1%; Pred. No. 2.5e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-NOV-2003.

(UYAR-) UNIV ARKANSAS MEDICAL SCI.

Query Match

Best Local Similarity 45.8%; Pred. No. 3.3e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39.8%; Score 547; DB 7; 46.1%; Pred. No. 2.5e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADC73287 standard, protein, 223 AA.
Bovine 2PTC E protein - SEQ ID 13.
W02003060765-A1.
24-JUL-2003.
(AJIN ) AJINOWOTO CO INC.
A (UMEY/) UMEYAMA H.
39.8%; Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADD35545 standard; protein; 223 AA. Cationic bovine trypsinogen TRY1. WO2003040093-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADI39734 standard, protein, 244 AA.
Human protease M (proM) protein.
US6642013-B1.
                                                                                                                                   AAY69973 standard; protein; 223 AA.
TRYP protein.
WO9962004-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY91925 standard, protein, 233 AA. Trypsinogen analogue. WO200017332-A1. 30-WAR-2000. (ELIL ) LILLY & CO ELI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADI37158 standard; protein; 244 AA.
Human protease m (Protm).
US2003199010-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR53637 standard; protein; 224 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 39.7%;
Best Local Similarity 45.8%;
RESULT 1178
Bovine TRYP peptide fragment JP10287696-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-MAY-1994.
(ELIL ) LILLY & CO ELI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-OCT-2003.
(UYAR-) UNIV ARKANSAS.
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity RESULT 1173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bovine trypsin.
EP597681-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-MAY-2003
                                                                                                                                                                                                                               Query Match
Best Local Si
RESULT 1171
                                                                              Query Match
Best Local Si
RESULT 1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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RESULT 1172
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Human Stratum Corneum Chymotryptic Enzyme, SCCE, catalytic domain. WO200129056-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39.7%; Score 545; DB 3; Length 246; 44.2%; Pred. No. 4e-34;
                                                                                               Length 247;
                                                                                                                                                                                                                                                         Length 247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 225,
AAY78974 standard; protein; 247 AA.

Canine cationic trypsinogen amino acid sequence.

WO20009739-A1.

24-FEB-2000.

A (FULY ) FULI YAKUHIN KOGYO KK.

Query Match
Best Local Similarity 45.6%; Pred. No. 3.3e-34;
                                                                                                                                                                                                                                                 Ouery Match 39.7%; Score 546; DB 6; Best Local Similarity 45.5%; Pred. No. 3.3e-34; RESULT 1180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 46.5%; Pred. No. 3.6e-34;
RESULT 1182
DE Canine anionic trypsinogen amino acid sequence.
PN W0200009739-Al.
PD 24-FEB-2000.
PA (FUJY ) FUJI YAKUHIN KOGYO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB98502 standard; protein; 225 AA.
                                                                                                                                                        ADA05742 standard; protein; 247 AA.
Human NOV18f protein SEQ ID NO:102.
WO2003029424-A2.
                                                                                                                                                                                                                                                                                                                  ADN62906 standard; protein; 247 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STONE D J.
PENA C E A.
SHENOY S G.
SHIMKETS R A.
ROTHENBERG M E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PATTURAJAN M.
SPYTEK K A.
EDINGER S R.
ELLERMAN K.
MALYANKAR U M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (EISE/) EISEN A.
(GANG/) GANGOLLI E A.
(RIEG/) RIEGER D K.
(SPAD/) SPADERNA S K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-APR-2001.
(UYAR-) UNIV ARKANSAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GORMAN L.
ZERHUSEN B D.
ANDERSON D W.
                                                                                                                                                                                                               10-APR-2003.
(CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LEACH M D.
AGEE M L.
BERGHS C.
DIPIPPO V A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZHONG M.
CATTERTON E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JI W.
MILLER C E.
RASTELLI L.
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WO9824886-A1
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                                                               Query Match
                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 1187
ID ADI16686 standard; protein; 259 AA.
DE Human NOVX protein to treat human pathological conditions SeqID222.
PN WO200268649-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39.3%; Score 539.5; DB 8; Length 259; 44.4%; Pred. No. 1.1e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 39.3%; Score 539.5; DB 5; Length 259. Local Similarity 44.4%; Pred. No. 1.1e-33;
                                                                           Length 257;
                                                                                                                                                                                                  Length 246;
                                                                                                                                                                                                                                                                                                                                       Length 220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 279;
                                                                                                                                                               Score 541; DB 7;
Pred. No. 7.2e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 541; DB 7;
Pred. No. 9.2e-34;
                                                                           DB 3;
                                                                                                             AAW64260 standard; protein; 246 AA.
Human amyloid beta-protein precursor inhibitor.
WO9824886-A1.
                                  WOZUUNCO...
14-SED-2000.
(MOUN) MOUNT SINAI HOSPITAL.
39.6%; Score 544; DB 3;
ery Match
^imilarity 44.1%; Pred. No. 5e-34;
                                                                                                                                                                                                                                                           Stereostructure-related 2PTC_E protein. WO2003060765-A1.
                                                                                                                                                                                                                                                                                                                                                                                ADC73301 standard; protein; 279 AA. Stereostructure-related 2PTC protein. WO2003060765-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 44.4%; Pred. RESULT 1189
ID ABB78122 standard; peptide; 223 AA.
AAB21326 standard; protein; 257 AA
                                                                                                                                                                                                                                            ADC73299 standard; protein; 220 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADN42340 standard; protein; 259 AA
                                                                                                                                                                                                                                                                                                                                     39.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                            24-JUL-2003.
(AJIN ) AJINOMOTO CO INC.
(UMEX/) UMEXAMA H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human novel proteinNOV 62
US2004033493-A1.
                                                                                                                                                                                                                                                                                                     (AJIN ) AJINOMOTO CO INC. (UMEY/) UMEYAMA H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COLMAN S D.
WOLENC A R.
PENA C E A.
GROSSE W M.
ALSOBROOK J P.
LEPLEY D M.
RIEGER D K.
BURGESS C E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GANGOLLI E A.
PADIGARU M.
ANDERSON D W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPYTEK K A.
ZERHUSEN B D.
PATTURAJAN M.
SHIMKETS R A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-SEP-2002.
(CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCHERNEV V T.
                                                                          Query Match
Best Local Similarity
RESULT 1184
                                                                                                                                                                                                           Best Local Similarity RESULT 1185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAUPIER R J. GUSEV V Y.
                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GERLACH V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MILLER C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RASTELLI
               Human HSCEE.
WO200053776-A2.
                                                                                                                                                                                                                                                                                          24-JUL-2003
                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ZERH/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (RAST/)
                                                                                                                                                                                                                                                                                                                                                                   RESULT 1186
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38.7%; Score 531.5; DB 5; Length 243; 43.8%; Pred. No. 4.3e-33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 6; Length 261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 37.8%; Score 519; DB 7; Length 232; RESULT 1197 ID ABG70276 standard; protein; 247 Ab DE Human Serine Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender Protease Trender P
                                                                                                                                            .Match 39.2%; Score 538; DB 5; Length 223; Local Similarity 45.6%; Pred. No. 1.2e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 516; DB 5; Length 247;
Pred. No. 6.9e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ID ABB04644 standard; protein; 240 AA.

DB Engraulis japonicus trypsinogen (aTry I) SEQ ID NO:1.

PD 02-0CT-2001.

PA (NISB ) JAPAN TOBACCO INC.

QUERY MATCh

Best Local Similarity 45.7%; Pred. No. 1.3e-32;

RESULT 1193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bovine SCCE protein N-terminal fragment SEQ ID 46.
WO200262135-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB84423 standard; peptide; 249 AA.
Murine SCCE protein N-terminal fragment SEQ ID 50.
WO200262135-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vuery Match
Best Local Similarity 40.0%; Pred. No. 3.9e-32;
RESULT 1196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BGHM ) BRIGHAM & WOMENS HOSPITAL.
ry Match
28.1%; Score 524; DB 2;
t Local Similarity 43.6%; Pred. No. 1.6e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 538; DB 5;
Pred. No. 1.2e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB84419 standard; peptide; 243 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human NOV13a protein; 261 AA. WO200290568-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW64261 standard; protein; 232 AA.
Kallikrein substrate binding site.
                                                                                                                                                                                                                                                                     ABB83322 standard; protein; 223 AA
Amino acid sequence of trypsin.
US2002072863-A1.
13-UIN-2002.
(FUIT ) FUJITSU LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              39.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37.6%;
                                                                                                                                                                                                                                                                                                             Partial trypsin sequence.
US2002035434-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-JUL-2002.
(CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-NOV-2002.
(CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                  21-MAR-2002.
(FUIT ) FUJITSU LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity RESULT 1194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
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Best Local Similarity
RESULT 1198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
RESULT 1192
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(EGEL/) EGELRUD T.
(HANS/) HANSSON L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 1195
ID ABR96164 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (EGEL/) EGELRUD T. (HANS/) HANSSON L.
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(WANG/)
(SKEI/)
(HEPL/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HEPL/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HEND/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (FANG/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CART/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HARL/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VEDV/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (KALO/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (RETT/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         risx/
                                                                                                                                                                                                                                                                                                                                                      PD 02-0CT-2001.
PA (NISB.) JAPAN TOBACCO INC.
Query Match
Best Local Similarity 45.9%; Pred. No. 5.6e-31;
RESULT 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PD 05-DEC-2002.
PA (INCYTE GENOMICS INC.
Query Match 36.5%; Score 501; DB 6; Length 261;
Best Local Similarity 43.3%; Pred. No. 1e-30;
RESULT 1205
                                                                                                                                                                                                                                                                                             Query Match 36.5%; Score 501; DB 5; Length 247; Best Local Similarity 43.3%; Pred. No. 9.8e-31; RESULT 1201
                                                                                                                                                                                                                                                                                                                                                                                 PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 36.5%; Score 501; DB 8; Length 247;
Best Local Similarity 43.3%; Pred. No. 9.8e-31;
RESULT 1202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            query Match 36.5%; Score 501; DB 8; Length 247; Beet Local Similarity 43.3%; Pred. No. 9.8e-31; RESULT 1203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
PA (SINO-) SINOGENOMAX CO LTD CHINESE NAT HUMAN GEN.
Query Match
Best Local Similarity 43.3%; Pred. No. 9.8e-31;
RESULT 1204
ID ABRA1530 standard; protein; 261 AA.
DE Human DITHP protein modification/maintenance protein.
PN WO200297031-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MOUN) MOUNT SINAI HOSPITAL.

ry Match 36.2%; Score 498; DB 3; Length 254; t Local Similarity 43.1%; Pred. No. 1.7e-30;
                                                       Query Match 37.4%; Score 514; DB 2; Length 268; Best Local Similarity 46.4%; Pred. No. 1.1e-31; RESULT 1199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    y.Match 36.4%; Score 500; DB 3; Length 223; Local Similarity 43.5%; Pred. No. 1.1e-30;
                                                                                                       LT 1199
ABBO4645 standard; protein; 241 AA.
Engraulis japonicus trypsinogen (aTry II) SEQ ID NO:2.
JP2001269173-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADQ30589 standard; protein; 247 AA.
Pancreas cancer marker - trypsin II precursor.
WO2004055519-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          D MON99594 standard; protein, 247 AA.

E Novel human protein sequence #410.

N W02004038003-A2.

D 06-MAY-2004.

A (FIVE-) FIVE PRIME THERAPEUTICS INC.

Query Match
                                                                                                                                                                                                                                                                                                                                                ADNO4140 standard; protein; 247 AA. Antipsoriatic protein sequence #265.WO2004028479-A2.
                                                                                                                                                                                                                                  AAU87693 standard; protein; 247 AA. Human pancreatic tumour protein #5. WO20021231-A2. (CORI-) CORIXA CORP.
AAW94493 standard; protein; 268 AA.
Human kallikrein.
WO9842849-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human neurosin amino acid sequence. WO200031284-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB21294 standard; protein; 254 AA.
Human KLK-L1 protein #2.
WO200053776-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB03862 standard; protein; 223 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-JUN-2000.
(FUSO ) FUSO PHARM IND LTD.
                                                01-OCT-1998
(INCY-) INCYTE PHARM INC.

    Best Local Similarity
    RESULT 1207

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Best Local Si
RESULT 1206
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PD 17-MAY-2001.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 43.1%; Pred. No. 1.7e-30;
RESULT 1210
                                                                               Length 254;
                                                                                                                                                                                                        Length 254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB95279 standard; protein; 254 AA.
Human P703P putative full length protein SEQ ID NO 525.
US2002022248-A1.
AAM01174 standard; protein; 254 AA.
Human prostate-specific amino acid sequence P703P.
W0200151633-A2.
19-JUL-2001.
(CORI-) CORIXA CORP.
                                                                                                                                                                                          Query Match 36.2%; Score 498; DB 4; Best Local Similarity 43.1%; Pred. No. 1.7e-30; RESULT 1209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36.2%; Score 498; DB 4; 43.1%; Pred. No. 1.7e-30;
                                                                               36.2%; Score 498; DB 4; 43.1%; Pred. No. 1.7e-30;
                                                                                                                                                                                                                                                      AAG99059 standard, protein; 254 AA.
Human prostate-specific amino acid of P703P.
WO200134802-A2.
                                                                                                                                                                                                                                                                                                                                                                               ABU71710 standard; protein; 254 AA.
Prostate cancer specific antigen P703P #7.
US2002192763-A1.
                                                                                                                            AAU69819 standard; protein; 254 AA.
Human prostate cDNA encoded protein #27.
WO200173032-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MCNE/) MCNEILL P D.
(HOUG/) HOUGHTON R L.
(DBAS/) Y DE BASSOLS C V.
(FOYT/) FOY T M.
                                                                                                                                                                                                                                                                                                                                                                                                                                              XU J.
DILLON D C.
MITCHAM J L.
HARLOCKER S L.
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WANG A.
SKEIKY Y A W.
HEPLER W T.
HENDERSON R A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LI S X.
WANG A.
SKEIKY Y A W.
HEPLER W T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DILLON D C.
MITCHAM J L.
HARLOCKER S L
                                                                                                                                                                         04-OCT-2001.
(CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DAY C H.
VEDVICK T S.
CARTER D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STOLK J A.
DAY C H.
VEDVICK T S.
CARTER D.
                                                                               Query Match
Best Local Similarity
RESULT 1208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JIANG Y.
KALOS M D.
FANGER G R.
RETTER M W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity RESULT 1211
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KALOS M D.
FANGER G R.
RETTER M W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STOLK J A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (DILL/)
(MITC/)
(HARL/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (KALO/)
(FANG/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SKEI/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HURA/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (DILL/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (JIAN/)
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PD 06-SEP-2002.

PA (CURA-) CURA-DORP.

Query Watch 36.2%; Score 497.5; DB 5; Length 230;

Best Local Similarity 47.4%; Pred. No. 1.7e-30;

RESULT 1221
                                                                                                                                                                                                                             Length 230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36.2%; Score 497.5; DB 8; Length 280; 42.7%; Pred. No. 2.1e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36.2%; Score 497.5; DB 8; Length 461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 230;
                                                                                    Score 498; DB 4; Length 1079; Pred. No. 7.6e-30;
                                                                                                                                    ADII17268 standard, protein; 230 AA.
Polypeptide homologous to a human NOVX domain SeqID 804.
WO200268649-A2.
                                                                                                                                                                                                                                                                         ADII1276 standard; protein; 230 AA.
Polypeptide homologous to a human NOVX domain SeqID 812.
WO200268649-A2.
                                                                                                                                                                                                                             5
                                                                                                                                                                                                                                                                                                                                                                                                            ADJ83075 standard; protein; 230 AA.
Trypsin-like serine protease protein - SEQ ID 66.
US2003170630-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36.2%; Score 497.5; DB 7; 47.4%; Pred. No. 1.7e-30;
                                                                                                                                                                                                                           Score 497.5; DB 5
Pred. No. 1.7e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Amino acid sequence of trypsinogen-Oaa-sp55.
WO2004019878-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T 1222
ADL27345 standard; peptide; 280 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amino acid sequence of trypsinogen. WO2004019878-A2.
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(COMP-) COMPOUND THERAPEUTICS INC.
(AFEY/) AFEYAN N B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADL27346 standard; peptide; 461 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-MAR-2004.
A (COMP-) COMPOUND THERAPEUTICS INC.
A (AFEX/) AFEXAN B. 36.2%; Score
Query Match
                                                                                    36.2%;
43.1%;
                                                                                                                                                                                        PD 06-SEP-2002.

PA (CURA-) CURAGEN CORP.

36.2%;

Best Local Similarity 47.4%;
(HURA/) HURAL J.
(MCNE/) MCNEILL P D.
(HOUG/) 'HOUGHTON R L.
(BDAS/) Y DE BASSOLS C V.
(FOYI/) FOY T M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GANGOLLI E A.
FERNANDES E R.
RIEGER D K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALSOBROOK J P. TCHERNEV V T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPYTEK K A.
ZERHUSEN B D.
PATTURAJAN M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SHIMKETS R A. GROSSE W M. SZEKERES E S. VERNET C A M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EDINGER S. R. GUNTHER E. MILLET I. SCIORE P. ELLERMAN K. MACDOUGALL J. SMITHSON G.
                                                                                   Query Match
Best Local Similarity
RESULT 1219
ID AD177268 standard; pr
DE Polypeptide homologou
PN W0200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CASMAN S J.
BOLDOG F L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
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BURGESS C E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GORMAN L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-SEP-2003
(ALSO/) ALSC
(TCHE/) TCHI
(LIUX/) LIU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match
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(SMIT/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SPYT/)
(ZERH/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SHIM/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SZEK/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CASM/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PATT/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GANG/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB74830 standard; protein; 1079 AA.
Prostate tumour antigen amino acid sequence for a fusion protein.
WO200125272-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1079;
                                                                                                                                                        Length 254;
                     Length 254;
                                                                                                                                                                                                                                                                                            Length 254;
                                                                                                                                                                                                                                                                                                                                                                                                                                 36.2%; Score 498; DB 6; Length 254; 43.1%; Pred. No. 1.7e-30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 254;
                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 43.1%; Pred. No. 1.7e-30;
RESULT 1214
ID ABR54391 standard; protein; 254 AA.

DB Prostate tumour specific protein sequence SEQ ID 525.
                   36.2%; Score 498; DB 5; 43.1%; Pred. No. 1.7e-30;
                                                                                                             03-0CT-2002.

(UYQU-) UNIV QUEENSLAND TECHNOLOGY.

ELY MAtch 36.2%; Score 498; DB 6;

ery Match 43.1%; Pred. No. 1.7e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36.2%; Score 498; DB 4; 43.1%; Pred. No. 7.6e-30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABU71860 standard; protein; 1079 AA.
Prostate specific antigen fusion protein #2.
US2002192763-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADG26391 standard; protein; 254 AA.
Human prostate-specific polypeptide #60.
US2003157089-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human prostate specific protein 254 AA. Human prostate specific protein P703P. 02-003185830-A1.
                                                                   ABP54360 standard; protein; 254 AA.
Human KLK4 protein SEQ ID NO:13.
WO200277243-A1.
                                                                                                                                                                                                  ABP54357 standard; protein; 254 AA. Human KLK4 protein SEQ ID NO:6. WO20027743-A1. 03-0CT-2002. (UYQU-) UNIV QUEENSLAND TECHNOLOGY.
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HARLOCKER S L.
JIANG Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STOLK J A.
DAY C H.
VEDVICK T S.
CARTER D.
LI S X.
WANG A.
SKEIKY Y A W.
HEPLER W T.
HENDERSON R A.
   (HEND/) HENDERSON R A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-OCT-2003.
(CORI-) CORIXA CORP.
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(CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-APR-2001.
(CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                              14-NOV-2002.
(CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                               it Local Similarity
IT 1215 ADB13975 standard; p:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                    Query Match
Best Local Similarity
RESULT 1213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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Best Local Similarity
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                                 Best Local Similarity
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DILLON D C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KALOS M D.
                                                                                                                                                                                                                                                                                                                                                                                WO200289747-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                     Query Match
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(HARL/)
(JIAN/)
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(HEND/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (KALO/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Loca
RESULT 1216
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RESULT 1217
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(SMIK ) SMITHKLINE BEECHAM BIOLOGICALS. (CORI-) CORIXA CORP.
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(CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-MAR-2003.
(CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity RESULT 1238
                                                  Best Local Similarity
RESULT 1233
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
RESULT 1236
                                                                                                                                                                  Query Match
Best Local Similarity
RESULT 1234
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RESULT 1241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity RESULT 1237
                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                       Length 464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 496.5; DB 2; Length 248; Pred. No. 2.2e-30;
                                                                                                                                                                                                                                                                                    DB 8; Length 485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 36.2%; Score 497; DB 5; Length 254; Beet Local Similarity 43.1%; Pred. No. 2.1e-30; RESULT 1231
                                                                                                                                                                                                                                                                                                                                                                                                              36.2%; Score 497; DB 3; Length 249; 43.1%; Pred. No. 2e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36.2%; Score 497; DB 3; Length 254; 43.1%; Pred. No. 2.1e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36.2%; Score 497; DB 4; Length 254; 43.1%; Pred. No. 2.1e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU74932 standard; protein; 254 AA.
AAuino acid sequence of prostase protein fragment #3.
WO200200867-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW60592 standard; protein; 248 AA.
Human prostate-specific kallikrein (HPSK) protein.
WO9820117-A1.
                                                                                                                                     Score 497.5; DB 8;
Pred. No. 3.5e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               O3-370-2002.
(SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
Query Match 36.2%; Score 497; DB 5;
                                                                                                                                                                                                                                                                                  36.2%; Score 497.5; DB 8 42.7%; Pred. No. 3.6e-30;
           42.7%; Pred. No. 3.5e-30;
                                                                                                                                                                                   ADL27348 standard; peptide; 485 AA.
Amino acid sequence of trypsinogen-20aa-sp55.
W02004019878-A2.
11-MAR-A2.
11-MAR-A2.
(ACOMP-) COMPOUND THERAPEUTICS INC.
(AFEY/) AFEYAN N B.
                                        ADL27347 standard; peptide; 464 AA.
Amino acid sequence of trypsinogen-3aa-sp55.
WO2004019878-A2.
11-MAR-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein sequence of protein; 254 AA.
Protein sequence of prostase homologue #3.
W02000708-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-JAN-2002.
(SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY72524 standard; protein; 248 AA.
Human prostase antigen #2.
WO200104143-A2.
18-JAN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA772525 standard; protein; 254 AA.
Human prostase antigen #3.
WO200104143-A2.
18-JAN-2001.
                                                                                                                                                                                                                                                                                                                                 AAB21307 standard; protein; 249 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB21320 standard; protein; 254 AA.
                                                                                                       (COMP-) COMPOUND THERAPEUTICS INC. (AFEY/) AFEYAN N B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human prostase.
WC20053776-A2.
14-SEP-2000.
(MOUN ) MOUNT SINAI HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                               (MOUN ) MOUNT SINAI HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36.1%;
                                                                                                                                       36.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (INCY-) INCYTE PHARM INC.
Best Local Similarity
RESULT 1224
                                                                                                                                       Ouery Match
Best Local Similarity
RESULT 1225
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity RESULT 1230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
RESULT 1226
                                                                                                                                                                                                                                                                                                                                                     Human prostase.
WO200053776-A2.
                                                                                                                                                                                                                                                                                                                                                                                  14-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loca
RESULT 1227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loca
RESULT 1229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Loca
RESULT 1232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best
RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BERGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22224
                                                                                                                                                                                         PADAGE
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36.0%; Score 494.5; DB 3; Length 247; 41.9%; Pred. No. 3.1e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36.0%; Score 494.5; DB 8; Length 246; 41.9%; Pred. No. 3.1e-30;
DB 4; Length 248;
                                                                                                                                                                                       Length 248;
                                                                                                                                                                                                                                                                                                                                                                                  Length 248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 5; Length 262;
                                                                                                                                                                                                                                                                                                                             PD 03-JAN-2002.

PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
Query Match
Best Local Similarity 43.4%; Pred. No. 2.2e-30;
RESULT 1235
ID ABG76997 standard; protein, 262 AA.
DE Human kallikrein protein variant #1.
PN W0200261131-A2.
PA (HULL) BRICKL-MYERS SQUIBB CO.
PA (HULL) HUI L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         uuery Match 36.0%; Score 494.5; DB 6;
Best Local Similarity 41.9%; Pred. No. 3.1e-30;
RESULT 1240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HOFF ) HOFFMANN LA ROCHE & CO AG F. (SINO-) SINOGENOMAX CO LTD CHINESE NAT HUMAN GEN. FY MAtch 136.0%; Score 494.5; DB 8; t Local Similarity 41.9%; Pred. No. 3.1e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 41.9%; Pred. No. 3.1e-30;
RESULT 1239
                                                                                                                                                                                       5;
                                                                                                                                                                                                                                                          AAU74931 standard; protein; 248 AA.
Amino acid sequence of prostase protein fragment
WO200200867-A1.
                                                                AATT4770 standard; protein; 248 AA.
Protein sequence of prostase homologue #2.
W0200200708-A2.
(SMT-2002.
(SMTK.) SMITHKLINE BEECHAM BIOLOGICALS.
ery Match
st Local Similarity 43.4%; Pred. No. 2.2e-30;
36.1%; Score 496.5; DB 4 43.4%; Pred. No. 2.2e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36.0%; Score 495; DB 5 40.4%; Pred. No. 3e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADQ30588 standard; protein; 247 AA.
Pancreas cancer marker - trypsin I precursor.
WO2004055519-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB21321 standard; protein; 247 AA. Human trypsinogen. WO200053776-A2. 14-SEP-2000. (MOUN ) MOUNT SINAI HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADR90673 standard, protein, 246 AA.
Human trypsinogen partial protein.
WO2004078777-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABRS4239 standard; protein; 247 AA.
Human NOV35a protein SEQ ID NO:146.
WO2003023001-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABR54241 standard; protein; 247 AA. Human NOV35c protein SEQ ID NO:150.WO2003023001-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAM01173 standard; protein; 254 AA.
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(BIOR-) BIOREXIS PHARM CORP.
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ADQ39654 standard; protein; 262 AA.
Human myocardial infarction-associated gene derived protein, SEQ ID 1317.
WO2004058052-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 40.4%; Score 494; DB 5; Length 262; RESULT 1251
ID ADLIS197 standard; protein; 262 AA.
DE Human pancreatic kallikrein.
9D 11.724.199-A.
                                                                                                                                                                                                                                                                                                                                                                PN WO200053776-A2.
PD 14-SEP-2000.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match
Best Local Similarity 40.4%; Pred. No. 3.6e-30;
RESULT 1250
36.0%; Score 494; DB 5; Length 254; 42.7%; Pred. No. 3.5e-30;
                                                                                                                                                                                                             Length 254;
                                                                                                                                                                                                                                                                                                               Query Match 36.0%; Score 494; DB 7; Length 254; Best Local Similarity 42.7%; Pred. No. 3.5e-30;
                                                                                                     Length 254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36.0%; Score 494; DB 7; Length 262; 40.4%; Pred. No. 3.6e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 494; DB 8; Length 262; Pred. No. 3.6e-30;
                 DE Prostate tumour specific protein; 254 AA.

PN W020028974-A2.

PD 14-NOV-2002.

PA (CORIX CORP.

Query Match

Best Local Similarity 42.7%; Pred. No. 2 F. 1.

PRESULT 1247
                                                                                                                                                                                                          36.0%; Score 494; DB 7; 42.7%; Pred. No. 3.5e-30;
                                                                                                                                        ADB13973 standard; protein; 254 AA.
Human mature prostate specific protein P703P.
US2003185830-A1.
                                                                                                                                                                                                                                               ADG26389 standard; protein; 254 AA.
Human prostate-specific polypeptide #59.
US2003157089-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-DEC-2002.
(REMI-) REMIN HOSPITAL SHENZHEN CITY
                                                                                                                                                                                                                                                                                                                                            IT 1249
AAB21319 standard; protein; 262 AA
Human KLK2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADL64969 standard; protein; 262 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABG76996 standard; protein; 262 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human kallikrein protein.
W0200261131-A2.
08-AUG-2002.
(BRIM ) BRISTOL-MYERS SQUIBB CO.
(TSUC.) TSUCHIHASHI Z.
(HUIL.) HUI L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human kallikrein protein (KLKI).
US2004033582-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POWELL J R.
RAMANATHAN C S.
SWANSON B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TSUCHIHASHI Z.
ZERBA K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-2004.
(APPL-) APPLERA CORP.
                                                                                                                                                                                                         Query Match
Best Local Similarity
RESULT 1248
                                                                                                                                                                                                                                                                                        21-AUG-2003.
(CORI-) CORIXA CORP.
                                                                                                                                                                                02-OCT-2003.
(CORI-) CORIXA CORP.
          Best Local Similarity RESULT 1246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity RESULT 1253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
RESULT 1252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HUI L.
PERRONE M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EDMONDS M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HUIL/)
(PERR/)
(POWE/)
(RAMA/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TSUC/)
                                                                                                                                                         Length 254;
                                                                                                                                                                                                                                                             Length 254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36.0%; Score 494; DB 4; Length 254; 42.7%; Pred. No. 3.5e-30;
                                                  Length 254;
Human prostate-specific amino acid mature form of P703P
                                                                                                                                                                                           AAGS9058 standard; protein; 254 AA.
Human prostate-specific mature protein of P703B.
WO200134802-A2.
                                                   36.0%; Score 494; DB 4; 42.7%; Pred. No. 3.5e-30;
                                                                                                                                                                                                                                                             36.0%; Score 494; DB 4; 42.7%; Pred. No. 3.5e-30;
                                                                                                                                                         Score 494; DB 4;
Pred. No. 3.5e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB95278 standard; protein; 254 AA.
Human P703P mature protein SEQ ID NO 523
                                                                                    Au69818 standard; protein; 254 AA.
Human prostate CDNA encoded protein #26.
04-001-3001.
(CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                    ABU71709 standard; protein; 254 AA.
Prostate cancer associated protein #12.
                                                                                                                                                       36.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HURA/) HURAL J.
(MCNE/) MCNEILL P D.
(HOUG/) HOUGHTON R L.
(BDAS/) Y DE BASSOLS C V.
(FOYT/) FOY T M.
                                                                                                                                                                                                                                                                                                                                                                   DILLON D C.
MITCHAM J L.
HARLOCKER S L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARTER D.
LI S X.
WANG A.
SKEIKY Y A W.
HEPLER W T.
HENDERSON R A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LI S X.
WANG A.
SKEIKY Y A W.
HEPLER W T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            STOLK J A.
DAY C H.
VEDVICK T S.
CARTER D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JIANG Y.
KALOS M D.
FANGER G R.
RETTER M W.
STOLK J. A.
DAY C H.
                                                                                                                                                     Query Match
Best Local Similarity
RESULT 1243
                       19-JUL-2001.
(CORI-) CORIXA CORP.
                                                                                                                                                                                                                                   17-MAY-2001.
(CORI-) CORIXA CORP.
                                                              Local Similarity
                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
RESULT 1244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MITCHAM J L.
HARLOCKER S
                                                                                                                                                                                                                                                                                                                                                                                                                      KALOS M D.
FANGER G R.
RETTER M W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            XU J.
DILLON D C.
                                                                                                                                                                                                                                                                                                                              JS2002192763-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                           JIANG Y.
                                                  Query Match
Best Local Si
RESULT 1242
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(WANG/)
(SKEI/)
(HEPL/)
(HEND/)
(HURA/)
                                                                                                                                                                                                                                                                                                                                                                     (DILL/)
(MITC/)
(HARL/)
(JIAN/)
(KALO/)
(FANG/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MITC/)
(HARL/)
(JIAN/)
(KALO/)
(FANG/)
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Best I
RESULT
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Best Local Similarity 40.4%; Pred. No. 4.3e-30; RESULT 1263
                                                                                                                                                                                                                                                                           Query Match 35.9%; Score 493.5; DB 6; Length 240;
Best Local Similarity 42.6%; Pred. No. 3.6e-30;
RESULT 1256
                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 3; Length 241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABP74111 standard; protein; 262 AA.
Human glandular kallikrein 1 precursor protein SEQ ID NO:600.
WO200281646-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery March 35.9%; Score 493; DB 8; Length 247; Best Local Similarity 42.1%; Pred. No. 4.1e-30; RESULT 1258
ID AAB21308 standard; protein; 253 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-DEC-2002.
11-DEC-2002.
(REMI-) REMIN HOSPITAL SHENZHEN CITY.
35.9%; Score 493; DB 7; Length 262;
       36.0%; Score 494; DB 8; Length 262; 40.4%; Pred. No. 3.6e-30;
                                                                                                                                                  Length 262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 493; DB 6; Length 262;
Pred. No. 4.3e-30;
                                            กบววสชม standard; protein; 262 AA.
Human autoimmune disease-related protein - SEQ ID 105.
WOZO4083403-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 40.4%; Pred. No. 3.6e-30;
RESULT 1255
DE Human trypsinogen protein; 240 AA.
DE Human trypsinogen protein SEQ ID No:341.
PN WO2003023301-A2.
PA (CURA-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               udery Match 35.9%; Score 493; DB 3; Best Local Similarity 42.8%; Pred. No. 4.2e-30; RESULT 1259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-JUL-1998.

(INCY-) INCYTE PHARM INC.

Query Match

15.9%; Score 493; DB 2;

Query Match

16.4%; Pred. No. 4.3e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                       35.9%; Score 493.5; DB 3 42.6%; Pred. No. 3.6e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WOZUUCZ...
14-SEP-2000.
(MOUN ) MOUNT SINAI HOSPITAL.
(ELY MATCh 35.9%; Score 493; DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADN04297 standard; protein; 247 AA. Antipsoriatic protein sequence #343 WO2004028479-A2.
                                                                                                                                                                                                                                                                                                                                                AAB21316 standard; protein; 241 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADL15204 standard, protein, 262 AA.
Pancreatic kallikrein #1.
CN1384199-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB21324 standard; protein; 258 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ) 17-OCT-2002.
(CTLI-) CTL IMMUNOTHERAPIES CORP.
Query Match 35.9%; Scor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200053776-A2.
14-SEP-2000.
(MOUN ) MOUNT SINAI HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                                                    (MOUN ) MOUNT SINAI HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-APR-2004.
(GETH ) GENENTECH INC
                                                                                                               30-SEP-2004.
(APPL-) APPLERA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity RESULT 1261
                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
RESULT 1257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
RESULT 1260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity RESULT 1262
       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                Human trypsinogen.
WO200053776-A2.
14-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human EMSP.
WO200053776-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human EMSP
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P P P P P
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AAB54293 standard; protein; 267 AA.
Human pancreatic cancer antigen protein sequence SEQ ID NO:745.
WO200055320-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             vuery Match 35.8%; Score 492; DB 2; Length 230; Best Local Similarity 43.7%; Pred. No. 4.5e-30; RESULT 1266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35.8%; Score 492; DB 1; Length 262; 40.4%; Pred. No. 5.2e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35.7%; Score 491; DB 5; Length 262; 40.4%; Pred. No. 6.2e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35.8%; Score 492; DB 3; Length 256; 41.1%; Pred. No. 5e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-SEP-2000.
(HUMA-) HUMAN GENOME SCI INC.
ery Match 35.8%; Score 492; DB 3; Length 267;
                                                                                                                     Length 263;
                                                                                                                                                                                                                                                                                                Length 225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 262;
ID ADM72846 standard; protein; 263 AA.

ID Human glandular kallikrein 1 protein SEQ ID NO:105.

BN WOO04022709-A2.

BD 18-WAR--2004.

PA (MANN-) MANNKIND CORP.

QUERY MACCh

BSST Local Similarity 40.4%; Pred. No. 4.3e-30;

RESULT 1264
                                                                                                                                                                                                                                                   PD 26-APR-2001.

PA (UYAR-) UNIV ARKANSAS.

Query Match 35.8%; Score 492; DB 4;
Best Local Similarity 43.7%; Pred. No. 4.4e-30;

RESULT 1265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35.8%; Score 492; DB 5; 40.4%; Pred. No. 5.2e-30;
                                                                                                                                                                                                       Human trypsin serine protease catalytic domain.
WO200129056-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAP95121 standard, protein, 262 AA.
Kallikrein encoded by clone lambda HK65a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABG77002 standard; protein; 262 AA.
Human kallikrein 1 polymorphic sequence
                                                                                                                                                                                                                                                                                                                                                               AAW39488 standard; protein; 230 AA.
Human TRYI trypsinogen variant protein.
WO9910503-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 40.4%; Pred. N
RESULT 1268
ID ABG76998 standard; protein; 262 AA.
BE Human kallikrein protein variant #2.
PN W0200261131-A2.
                                                                                                                                                                                    AAB98503 standard; protein; 225 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB21315 standard; protein; 256 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADA05744 standard; protein; 224 AA.
Human NOV18g protein SEQ ID NO:104.
WO2003029424-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BRIM) BRISTOL-MYERS SQUIBB CO. (TSUC/) TSUCHIHASHI Z. (HUIL/) HUI L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BRIM ) BRISTOL-MYERS SQUIBB CO. (TSUC/) TSUCHIHASHI Z. (HUIL/) HUI L.
                                                                                                                                                                                                                                                                                                                                                                                                                                      04-MAR-1999.
(HOFF ) ROCHE DIAGNOSTICS GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200053776-A2.
14-SEP-2000.
(MOUN ) MOUNT SINAI HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
RESULT 1270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
RESULT 1267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EP297913-A.
04-JAN-1989.
(AMGE-) AMGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200261131-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human KLK1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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Score 487.5; DB 4; Length 449; Pred. No. 2e-29;
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                                                                                                                                                                                     Query Match 35.5%; Score 487.5; DB 4; Length 449; Best Local Similarity 44.1%; Pred. No. 26-29; RESULT 1278
                                                                                                                                                                                                                                                                                                                    Length 449;
                                                   (FIVE-) FIVE PRIME THERAPEUTICS INC.
ry Match 35.5%; Score 488; DB 8; Length 247;
t Local Similarity 42.3%; Pred. No. 9.9e-30;
                                                                                                                                                                                                                                                                                                                                                             ABU71763 standard; protein; 449 AA.
Prostate cancer specific antigen fusion protein #1.
US2002192763-A1.
                                                                                                                                                                                                                                         AAU69872 standard; protein; 449 AA.
Human prostate serum antigen/P703P fusion protein.
WO200173032-A2.
                                                                                                                                                                                                                                                                                                                      4 ;
                                                                                                                                                                                                                                                                                                                    35.5%; Score 487.5; DB 44.1%; Pred. No. 2e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB95332 standard; protein; 449 AA.
Human P703P/PSA fusion protein SEQ ID NO 617.
US2002022248-A1.
                                                                                                             AAM01227 standard; protein; 449 AA.
P703P and PSA fusion amino acid sequence.
W020015151633-A2.
19-JUL-2001.
(CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35.5%;
44.1%;
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HOUGHTON R L.
Y DE BASSOLS C V.
FOY T M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (STOL/) STOLK J A.
(DAYC) DAY C H.
(VEDV/) CARTER D.
(LISX/) LI S X.
(MAMG/) WANG A.
(SKEIX/) SKEIXY Y A W.
(HEPL/) HEPLER W T.
(HEDL/) HEPLER W T.
                                                                                                                                                                                                                                                                                                                                                                                                                                XU J.
DILLON D C.
MITCHAM J L.
HARLOCKER S L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WANG A.
SKEIKY Y A W.
HEPLER W T.
HENDERSON R A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MITCHAM J L.
HARLOCKER S L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STOLK J A.
DAY C H.
VEDVICK T S.
CARTER D.
                                                                 Query Match
Best Local Similarity
RESULT 1277
                                                                                                                                                                                                                                                                                       04-OCT-2001.
(CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
RESULT 1279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JIANG Y.
KALOS M D.
FANGER G R.
RETTER M W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KALOS M D.
FANGER G R.
RETTER M W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match
Local Similarity
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DILLON D C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
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                                         06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                  19-DEC-2002
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(DILL/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (FANG/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MANG/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HURA/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 1280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (JIAN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KALO/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FANG/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35.6%; Score 489.5; DB 4; Length 234; 43.0%; Pred. No. 7.2e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 35.5%; Score 488; DB 8; Length 247; Best Local Similarity 42.3%; Pred. No. 9.9e-30; RESULT 1276
                                                                     Length 224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35.6%; Score 488.5; DB 2; 43.9%; Pred. No. 8.4e-30;
                                                                   / Match 35.7%; Score 490; DB 6; Local Similarity 45.3%; Pred. No. 6.3e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35.7%; Score 490; DB 8; 45.3%; Pred. No. 6.3e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY25510 standard; protein; 231 AA.
Human prostate serine protease protein.
EP936270-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADNO4726 standard, protein; 247 AA. Antipsoriatic protein sequence #544.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE00397 standard; protein; 234 AA.
Human serine protease, PROST 07.
WO200125446-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADN99593 standard; protein; 247 AA.
Novel human protein sequence #409.
WO2004038003-A2.
                                                                                                                ADN62908 standard; protein; 224 AA.
Human NOV18g.
US2004038223-A1.
PD 10-APR-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Siminares
                                                                                                                                                                                                                                                                      GUO X.
PATTURAJAN M.
SPYTEK K A.
                                                                                                                                                                                                                                                                                                                      EDINGER S R.
ELLERMAN K.
MALYANKAR U M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LEACH M D.
AGEE M L.
BERGHS C.
DIPIPPO V A.
EISEN A.
GANGOLLI E A.
REGER D K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PENA C E A.
SHENOY S G.
SHIMKETS R A.
ROTHENBERG M E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-APR-2004.
(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                GORMAN L.
ZERHUSEN B D.
ANDERSON D W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PD 18-AUG-1999.
PA (BADI ) BASF AG.
Query Match
Best Local Similarity
RESULT 1275
                                                                                                                                                                                             MILLET I.
PEYMAN J A.
KEKUDA R.
                                                                                                                                                                                                                                                                                                                                                                                                                                ZHONG M.
CATTERTON E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SCHD ) SCHERING AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
RESULT 1274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MILLER C E.
RASTELLI L.
STONE D J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity RESULT 1273
                                                                                                                                                                             SMITHSON G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                JI W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (EISE/)
(GANG/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SPAD/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (RIEG/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PENA/)
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                                                                                                                                                                                               MILL/
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HENDERSON R A.
HURAL J.
MUNEILL P D.
HOUGHTON R L.
Y DE BASSOLS C V.
FOY T M.
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HEPLER W T.
HENDERSON R A.
                                                                                                                                                                                                                                                                                                                                                                                                     XU J.
DILLON D C.
MITCHAM J L.
HARLOCKER S L.
                                                                                                                                                                                                                                      Query Match
Best Local Similarity
RESULT 1288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STOLK J A.
DAY C H.
VEDVICK T S.
CARTER D.
LI S X.
WANG A.
                                                                                                                                                                                                                     02-OCT-2003.
(CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HURAL J.
MCNEILL P D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   KALOS M D.
FANGER G R.
RETTER M W.
                                                                     Query Match
Best Local Similarity
RESULT 1286
                                                                                                                                                                                                                                                                                                                                  Best Local Similarity RESULT 1289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
RESULT 1291
HEPLER W T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FOY T M.
                                                                                                                                                                                                                                                                                                                                                                                          9-DEC-2002
                           (MCNE/) (HOUG/) (DBAS/) (FOYT/)
                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (DBAS/)
(FOYT/)
                   (HURA/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HURA/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                    HARL/)
                                                                                                                                                                                                                                                                                                                                                                                                                                              JIAN/
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(HEPL/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HEND/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FANG/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VEDV/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LISX/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STOL/
                                                                                                                                              35.5%; Score 487.5; DB 7; Length 449; 44.1%; Pred. No. 2e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35.5%; Score 487.5; DB 4; Length 585; 44.1%; Pred. No. 2.6e-29;
                                                            Length 449;
                                                                                                                                                                                                                               35.5%; Score 487.5; DB 7; Length 449; 44.1%; Pred. No. 2e-29;
                                                                                 AUB14067 standard; protein; 449 AA.
Human prostate specific protein P703P/PSA fusion protein.
US2003185330-A1.
      ABU71889 standard; protein; 585 AA.
Prostate cancer specific antigen fusion protein #3.
US2002192763-A1.
                                                           35.5%; Score 487.5; DB 6; 44.1%; Pred. No. 2e-29;
                                                                                                                                                                           ADG26483 standard; protein; 449 AA.
Human prostate-specific polypeptide #113.
US2003157089-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABU71888 standard; protein; 585 AA.
Prostate cancer associated protein #72.
US2002192763-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                  (LISX/) LI S X.
(WANG/) WANG A.
(WEDL/) SKEIKY Y A W.
(HEPL/) HEPLER W T.
(HEND/) HENDERSON R A.
(HURA/) HURAL J.
(MCNE/) MCNEILL P D.
(HOUG/) HOUGHPAORSON R L.
(HORA)/ Y DE BASSOLS C V.
(FOYI/) FOY T M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DILLON D C.
MITCHAM J L.
HARLOCKER S L.
                                                                                                                                                                                                                                                                                                                             MITCHAM J L.
HARLOCKER S L.
                                                                                                                                                                                                                                                                                                                                                                                         STOLK J A.
DAY C H.
VEDVICK T S.
CARTER D.
                                                                                                                       02-OCT-2003.
(CORI-) CORIXA CORP.
                                                                                                                                                                                                          21-AUG-2003.
(CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JIANG Y.
KALOS M D.
FANCER G R.
STOLK J A.
DAY C H.
VEDVICK T S.
CARTER D.
LI S X.
WANG A.
                                                                                                                                           Query Match
Best Local Similarity
RESULT 1283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SKEIKY Y A W
                                                                                                                                                                                                                              Query Match
Best Local Similarity
RESULT 1284
                                                          Query Match
Best Local Similarity
RESULT 1282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                  DILLON D C.
                                                                                                                                                                                                                                                                                                                                                JIANG Y.
KALOS M D.
                                                                                                                                                                                                                                                                                                                                                                     FANGER G R.
RETTER M W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Si
RESULT 1285
                                                                                                                                                                                                                                                                                                                                      (HARL/)
(JIAN/)
                                                                                                                                                                                                                                                                                                                                                                     (FANG/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (JIAN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (WANG/)
(SKEI/)
                                                                                                                                                                                                                                                                                                                                                            KALO/)
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RESULT 1281
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Score 487.5; DB 4; Length 585; Pred. No. 2.6e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 487.5; DB 4; Length 801;
Pred. No. 3.6e-29;
                                                                                                                                                                      Length 585;
                                                                                                                                                                                                                                                                                                                                          35.5%; Score 487.5; DB 7; Length 585; 44.1%; Pred. No. 2.6e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35.5%; Score 487.5; DB 7; Length 585; 44.1%; Pred. No. 2.6e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 487; DB 2; Length 224;
Pred. No. 1.1e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABU71890 standard; protein; 801 AA.
Prostate cancer specific antigen fusion protein #4
US2002192763-A1.
                                                                                                                                                                      9
                                                                                                              PD 14-NOV-2002.

PA (CORI-) CORIXA CORP.

Query March

Best Local Similarity 44.1%; Pred. No. 2.6e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 44.1%; Pred. No. 3.6e-2 RESULT 1290

ID AAY31160 standard; protein; 224 AA.

DE Human trypsin serine protease protein domain. PN USS948892-A.

PD 07-SEP-1999.

PA (AMGE-) AMGEN INC.
                                                            ABR54580 standard; protein; 585 AA.
Prostate tumour-related protein SEQ ID 1020.
WO200289747-A2.
                                                                                                                                                                                                                                                                                                                                                                                                       ADG26993 standard; protein; 585 AA.
Human prostate-specific polypeptide #249.
22003157089-A1.
21-AUG-2003.
(CORI-) CORIXA CORP.
                                                                                                                                                                                                                                ADB14470 standard; protein; 585 AA. FOPP/hPAP fusion protein, FOPP3. US2003185830-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADL15207 standard; protein; 261 AA.
Pancreatic kallikrein #3.
35.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HOUGHTON R L.
Y DE BASSOLS C V.
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WO200200708-A2.
                     03-JAN-2002
(SMIK ) SMJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HURA/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JIAN/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LISX/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HEPL/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HEND)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery
              11-DEC-2002.
(REMI-) REMIN HOSPITAL SHENZHEN CITY.
ery Match 35.3%; Score 484.5; DB 7; Length 261;
-- '--- Similarity 40.2%; Pred. No. 1.9e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 483.5; DB 2; Length 240;
Pred. No. 2.1e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14.SEP-2000.
(MOUN) MOUNT SINAI HOSPITAL.
ery Match 35.1%; Score 482.5; DB 3; Length 237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SMIK) SMITHKLINE BEECHAM PLC.
Query Match
34.8%; Score 477.5; DB 4; Length 216;
Best Local Similarity 44.3%; Pred. No. 5.5e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 477.5; DB 4; Length 226;
Pred. No. 5.8e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35.0%; Score 481; DB 1; Length 262; 40.0%; Pred. No. 3.6e-29;
                                                                                                                                                                                                                                                                                                                                                                                        Length 333;
                                                                                                                                                                                                                           Length 261
                                                                                                              ABM83249 standard; protein; 261 AA.
Human diagnostic and therapeutic pprotein SEQ ID NO:3498.
WO2004023973-A2.
25-WAR.2004.
(INCY-) INCYTE CORP.
                                                                                                                                                                                                                                                                                ABMG3250 standard, protein; 333 AA.

Human diagnostic and therapeutic pprotein SEQ ID NO:3499.

WQ2004023973-A2.

2.5-MAR-2004.

(INNY-) INCYTE CORP.

35.2%; Score 484; DB 8; Length 33 Best Local Similarity 43.5%; Pred. No. 2.7e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAP70568 standard; protein; 262 AA.
Human kallikrein-like substance has hypotensive activity.
JP62126980-A.
                                                                                                                                                                                                                         Score 484; DB 8;
Pred. No. 2.1e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PD 11-DEC-2002.
PA (REMI-) REMIN HOSPITAL SHENZHEN CITY.
Query Match 35.2%; Score 483; DB 7;
BEST Local Similarity 39.8%; Pred. No. 2.5e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU74902 standard; protein; 226 AA.
Protein sequence of prostase homologue #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY72526 standard; protein; 226 AA.
Human prostase antigen P703PDE5 sequence.
WO200104143-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-JAN-2001.
(SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
(CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADL15206 standard; protein; 260 AA.
Pancreatic kallikrein #2.
CN1384199-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB21293 standard; protein; 237 AA.
Human KLK-L1 protein #1.
WO200053776-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU01290 standard; protein; 216 AA.
Human serine protease HETAA37p.
WO200123587-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW57740 standard; protein; 240 AA.
                                                                                                                                                                                                                         35.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 35.2%;
Best Local Similarity 42.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Trypsinogen-like protein. JP10099080-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-APR-1998.
(SHIS ) SHISEIDO CO LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-JUN-1987.
(NAKA/) NAKANISHI S.
                                                                          Best Local Similarity RESULT 1292
                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
RESULT 1300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity RESULT 1299
CN1384199-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-APR-2001
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                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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DE Amino acid sequence of protein; 226 AA.

DE Amino acid sequence of prostase protein fragment #4.

PN WO200200867-A1.

PD 03-JAN-2002.

PD 03-JAN-2002.

PA (SMIX ) SMITHKLINE BEECHAM BIOLOGICALS.

Query Match

Query Match

Best Local Similarity 43.8%; Pred. No. 5.8e-29;

RESULT 1302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU74929 standard; protein; 312 AA.
Amino acid sequence of wild-type NSI-P703P-His fusion protein.
WO200200867-Al.
SMITHKLINE BEECHAM BIOLOGICALS.

A 34.8%; Score 477.5; DB 5; Length 226; Similarity 43.8%; Pred. No. 5.8e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34.8%; Score 477.5; DB 4; Length 344; 43.8%; Pred. No. 8.9e-29;
                                                                                                                                                                                                                                                                                                                                      Length 312;
                                                                                                                                                                                                                                                                                                                                                                                      AAU74768 standard; protein; 312 AA.
Amino acid sequence of wild-type NS1-p703-His fusion protein.
WO200200708-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABM82601 standard; protein; 239 AA.
Human diagnostic and therapeutic pprotein SEQ ID NO:2850.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABU71886 standard; protein; 344 AA.
Human prostate specific antigen (PSA) epitope #26.
US2002192763-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 34.8%; Score 477.5; DB 5; 43.8%; Pred. No. 8.1e-29;
                                                                                                                                                                                                                                                                                                                                        34.8%; Score 477.5; DB 4; 43.8%; Pred. No. 8.1e-29;
                                                                                                                                                                                                                                                                                                 (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS. (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-JAN-2002.
(SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                                                                                                                                                                                         AAY72522 standard; protein; 312 AA. NSI-P703P-His fusion protein. WO200104143-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HENDERSON R A.
HURAL J.
MUNBILL P D.
HOUGHTON R L.
Y DE BASSOLS C V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LI S X.
WANG A.
SKEIKY Y A W.
HEPLER W T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DILLON D C.
MITCHAM J L.
HARLOCKER S L
                                                                                                                                                                                                                                                                                                                                        Match
Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2004023973-A2.
25-MAR-2004.
(INCY-) INCYTE CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DAY C H.
VEDVICK T S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
RESULT 1306
                                  Best Local Similarity
RESULT 1301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
RESULT 1305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FANGER G R.
RETTER M W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KALOS M D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STOLK J A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARTER D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JIANG Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-DEC-2002
                                                                                                                                                                                                                                                                                   18-JAN-2001
                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match
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                                                                                                                                                                                                                                                                                                                                                           Best Loca
RESULT 1303
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Best Local Similarity 43.8%; Pred. No. 1.4e-28; RESULT 1316
                                                                                                                                                                                            KALOS M D.
FANGER G R.
RETTER M W.
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FANGER G R.
RETTER M W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-NOV-2002.
(CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
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RESULT 1320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match
Local Similarity
                                                                                                                                                                                                                                             STOLK J A.
DAY C H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STOLK J A.
DAY C H.
VEDVICK T S
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                                                                                                                                                                                JIANG Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JIANG Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      (DBAS/)
(FOYT/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Matc
Best Local
RESULT 1317
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                                                                                                                                                                                (JIAN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                      HOUG/
                                                                                                                                                                                                               FANG/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (WANG/
                                                                                                                                                                                                                                                                                                                                                                                                                      MCNE/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JIAN/
                                                                                                                                                                                                                                                                                                                                                                                       HEND/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LISX/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SKEI/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Prostate tumour antigen predicted amino acid sequence for P703PDE5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY82008 standard; protein; 220 AA.
Human immunogenic prostate tumour protein sequence SEQ ID NO:327.
WO200004149-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34.4%; Score 472.5; DB 4; Length 220; 43.8%; Pred. No. 1.4e-28;
                                                                                                                                                                                                                                                                                 34.6%; Score 475.5; DB 8; Length 239; 40.1%; Pred. No. 8.8e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34.4%; Score 472.5; DB 3; Length 220; 43.8%; Pred. No. 1.4e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34.4%; Score 472.5; DB 4; Length 220; 43.8%; Pred. No. 1.4e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34.4%; Score 472.5; DB 4; Length 220;
            Length 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 220;
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Pred. No. 1.4e-28;
                                                                                                                                            Length 239,
                                                                                                                                                                                                                                                                                                                                                                                                                     Length 280;
                                                                                                                                                                                          ABM82603 standard; protein; 239 AA.
Human diagnostic and therapeutic pprotein SEQ ID NO:2852.
WO2004023973-A2.
                                                                         Human diagnostic and therapeutic pprotein SEQ ID NO:2851 WO2004023973-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AMGSYMUB Standard; protein; 220 AA.
Human prostate-specific amino acid sequence P703PDES.
W0200134802-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAM01123 standard; protein; 220 AA.
Human prostate-specific amino acid sequence P703PDE6
WO200151633-A2.
            34.6%; Score 475.5; DB 8; 40.1%; Pred. No. 8.8e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4;
                                                                                                                                            Score 475.5; DB 8;
Pred. No. 8.8e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 472.5; DB 4
Pred. No. 1.4e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                     Score 473; DB 8;
Pred. No. 1.6e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG62147 standard; protein; 220 AA.
Human P703P inventive antigen SEQ ID NO: 330.
WO200125273-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU69768 standard; protein; 220 AA.
Human prostate cDNA encoded protein #8
WO200173032-A2.
                                                                                                                                                                                                                                                                                                                                                                                                     (FIVE-) FIVE PRIME THERAPEUTICS INC.
                                                                                                                                                                                                                                                                                                                       Novel human protein sequence #465. 06-May.
                                                               protein; 239 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB74806 standard; protein; 220 AA
                                                                                                                                              34.6%;
40.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                      34.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34.4%;
43.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-APR-2001.
(CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-APR-2001.
(CORI-) CORIXA CORP.
Query Match
                                                                                                             25-MAR-2004.
(INCY-) INCYTE CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CORI-) CORIXA CORP.
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-JUL-2001.
(CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-OCT-2001.
CORI-) CORIXA CORP.
Query Match
Best Local Similarity
                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                               25-MAR-2004.
(INCY-) INCYTE CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-MAY-2001.
(CORI-) CORIXA CORP.
            Query Match
Best Local Similarity
RESULT 1307
                                                                                                                                                                                                                                                                                               Best Local Similarity
RESULT 1309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                           ABM82602 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                       06-MAY-2004
                                                                                                                                                                                                                                                                                  Query Match
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Score 472.5; DB 4; Length 220; Pred. No. 1.4e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 472.5; DB 7; Length 220; Pred. No. 1.4e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34.4%; Score 472.5; DB 6; Length 220; 43.8%; Pred. No. 1.4e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABRS4340 standard; protein; 220 AA.
Prostate tumour specific protein sequence SEQ ID 327.
WO200289747-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 472.5; DB 5;
Pred. No. 1.4e-28;
ABU71659 standard; protein; 220 AA.
Prostate cancer specific antigen P703P #4.
US2002192763-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LT 1319
DBD13777 standard; protein; 220 AA.
Human prostate specific protein P703PDES.
US2003185830-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADG26193 standard; protein; 220 AA.
Human prostate-specific polypeptide #9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB95228 standard; protein; 220 AA.
Human P703PDES protein SEQ ID NO 327.
US2002022248-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  34.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 43.8%;
RESULT 1318
                                                                                                                                                                                                                                                                                                                                                              HURAL J.
MCNEILL P D.
HOUGHTON R L.
Y DE BASSOLS C V.
FOY T M.
                                                                                                                                                                                                                                                                           LI S X.
WANG A.
SKEIKY Y A W.
HEPLER W T.
HENDERSON R A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        XU J.
DILLON D C.
MITCHAM J L.
HARLOCKER S L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LI S X.
WANG A.
SKEIKY Y A W.
HEPLER W T.
                                                                                  DILLON D C.
MITCHAM J L.
HARLOCKER S L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HENDERSON R A.
                                                                                                                                                                                                                                       VEDVICK T S.
CARTER D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-OCT-2003.
(CORI-) CORIXA CORP.
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17-CCT-2002.
(CTLI-) CTL IMMUNOTHERAPIES CORP.
(ery Match 34.2%; Score 470.5; DB 6; Length 261;
(ery Match 40.4%; Pred. No. 2.3e-28;
                                                                                                                                                 14.SEP-2000.

14.SEP-2000.

(MOUN ) MOUNT SINAI HOSPITAL.

34.2%; Score 470.5; DB 3; Length 261;

lery Match

34.2%; Score 470.5; DB 3; Length 261;

16.1%; Score 470.5; DB 3; Length 261;
    PA (ENTR-) ENTREMED INC.
Query Match;
Best Local Similarity 40.4%; Pred. No. 2.3e-28;
RESULT 1330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34.2%; Score 470.5; DB 4; Length 261; 40.4%; Pred. No. 2.3e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 261;
                                                                                                                                                                                                                                                                                                                                                             Length 261;
                                                                                                                                                                                                                                                                                                                                                                                                     ANG62144 standard; protein; 261 AA.
Human prostate specific membrane antigen SEQ ID NO: 327.
W020012523-A2.
                                                                                                                                                                                                                                                          AAB74821 standard; protein; 261 AA.
Prostate tumour antigen amino acid sequence for PSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 34.2%; Score 470.5; DB 4;
Best Local Similarity 40.4%; Pred. No. 2.3e-28;
                                                                                                                                                                                                                                                                                                                                                             34.2%; Score 470.5; DB 4; 40.4%; Pred. No. 2.3e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABUT1859 standard, protein; 261 AA.
Human prostatic specific membrane antigen (PSMA).
US2002192763-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 34.2%; Score 470.5; DB 4 Best Local Similarity 40.4%; Pred. No. 2.3e-28; RESULT 1334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAG62146 standard; protein; 261 AA.
Human prostate specific antigen SEQ ID NO: 329.
WO200125273-A2.
                                                                                          AAB21317 standard; protein; 261 AA.
Human PSA.
WO200053776-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .r 1335
ABP74202 standard; protein; 261 AA.
Human PSA protein SEQ ID NO:78.
WO200281646-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LISX.
WANGA.
SKEIKY Y A W.
HEPLER W T.
HENDERSON R A.
HURAL J.
MCNEILL P D.
HOUGHTON R L.
Y DE BASSOLS C V.
FOY T M.
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MITCHAM J L.
HARLOCKER S L.
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DAY C H.
VEDVICK T S.
CARTER D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-APR-2001.
(CORI-) CORIXA CORP.
                                                                                                                                                                                             Query Match
Best Local Similarity
RESULT 1331
ID AAB74821 standard; p
                                                                                                                                                                                                                                                                                                WO200125272-A2.
12-APR-2001.
(CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity RESULT 1332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-APR-2001.
(CORI-) CORIXA CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KALOS M D.
FANGER G R.
RETTER M W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JIANG Y.
02-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (FANG/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (KALO/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (JIAN/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CART/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SKEI/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PD 02-DEC-1999.

PA (UYPE-) UNIV PENNSYLVANIA.

Query Match

Best Local Similarity 40.4%; Pred. No. 2.3e-28;

RESULT 1329
                                                                                                                                                                                                                                                                                                                                                               Query Match 34.4%; Score 472.5; DB 8; Length 262; Best Local Similarity 38.9%; Pred. No. 1.6e-28; RESULT 1323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 472.5; DB 6; Length 274; Pred. No. 1.7e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34.2%; Score 470.5; DB 4; Length 257; 40.4%; Pred. No. 2.3e-28;
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4 (WORCE) WORCESTER FOUND BIOMEDICAL RES.

Query Match

34.2%; Score 470.5; DB 2; Length 261;

Best Local Similarity 40.4%; Pred. No. 2.3e-28;
                                                        34.4%; Score 472.5; DB 7; Length 220; 43.8%; Pred. No. 1.4e-28;
                                                                                                                                                                                                                  Query Match 34.4%; Score 472.5; DB 8; Length 262; Best Local Similarity 38.9%; Pred. No. 1.6e-28; RESULT 1322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34.2%; Score 470.5; DB 3; Length 255; 40.4%; Pred. No. 2.3e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34.3%; Score 471; DB 1; Length 245; 40.2%; Pred. No. 2e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY77842 standard; protein; 261 AA.
Human prostate-specific antigen (PSA) sequence.
WO9960984-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU06276 standard; protein; 257 AA.
Prostate specific Antigen (PSA) polypeptide.
WO200145728-A2.
                                                                                                                                                                                                                                                                             ADI37156 standard, protein, 262 AA. Human glandular kallikrein (hHk2) protein. US2003199010-A1. 23-OCT-2003. (UYAR-) UNIV ARKANSAS.
                                                                                          RESULT 1321
ID ADI39732 standard; protein; 262 AA.
DE Human glandular kallikrein (HK2) protein.
PN US6642013-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                           ABR96163 standard; protein; 274 AA.
Human NOV12a protein SEQ ID NO:68.
WO200290568-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAP92314 standard; protein; 245 AA.
Human recombiant kallikrein gene.
EP297913-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW13649 standard; protein; 261 AA. Human prostatic specific antigen. W09711172-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB21313 standard; protein; 255 AA. Human PSA. WO200053776-A2. (MOUN ) MOUNT SINAI HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAYS6048 standard; protein; 261 AA.
Human prostate-specific antigen.
WO9961068-A1.
                                                                                                                                                                          04-NOV-2003.
(UYAR-) UNIV ARKANSAS MEDICAL SCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PD 14-NOV-2002.

PA (CURA-) CURAGEN CORP.

QUETY MATCh

BEST Local Similarity 40.7%;

RESULT 1324
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PA (AMGE-) AMGEN.
Query Match
Best Local Similarity RESULT 1325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PD 28-JUN-2001.
PA (EPIM-) EPIMMUNE INC.
QUEYY MATCh
Best Local Similarity
RESULT 1327
                     21-AUG-2003.
(CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
RESULT 1326
                                                      Query Match
Best Local Similarity
US2003157089-A1.
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PENE

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protein; 261 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-JUL-1995.
(SANY) SANKYO CO LTD.
Query Match 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
RESULT 1350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
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Best Local Similarity
RESULT 1348
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                                                                                                                                                  ADJ59024 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABM82166 standard; protein; 261 AA.
Tumour-associated antigenic target (TAT) polypeptide PRO2109, SEQ:5591.
WO2004030615-A2.
ADB82777 standard; protein; 261 AA.
Human protein sequence useful for the treatment of cancer (SeqID 1558).
W0200350236-A2.
19-JUN-2003.
(CHIR ) CHIRON CORP.
(HYSE) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                   Length 261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 8; Length 261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34.2%; Score 470.5; DB 3; Length 375; 40.4%; Pred. No. 3.4e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34.2%; Score 470.5; DB 4; Length 692; 40.4%; Pred. No. 6.3e-28;
                                                                                                                 Score 470.5; DB 7; Length 261;
Pred. No. 2.3e-28;
                                                                                                                                                                                                                                                                    Length 261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 470.5; DB 8; Length 261;
Pred. No. 2.3e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 470.5; DB 8; Length 261; Pred. No. 2.3e-28;
                                                                                                                                                                                                                   J4.2%; JSCOTE 470.5; DB 7;

LU ADD3922 standard; protein; 261 AA.

DE Human PSA precursor protein; 261 AA.

PN W02003047506-A2.

PD 12-UN-2003.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

Query Match

BEST Local Similarity 40.4%; Pred. No. 2.3e-28;

RESULT 1339

ID AD199733 standard; protein; 261 AA.

PN US6642013-B1.

PD 04-NOV-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB08449 standard; protein; 375 AA.
A human prostate specific antigen variant polypeptide.
WO200049158-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34.2%; Score 470.5; DB 8 40.4%; Pred. No. 2.3e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34.2%; Score 470.5; DB 8 40.4%; Pred. No. 2.3e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAG62154 standard; protein; 692 AA.
Human WT1/PSA fusion protein SEQ ID NO: 357.
WO200125273-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADI37157 standard; protein; 261 AA.
Human prostate specific antigen (hPSA).
US2003199010-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADM72819 standard; protein; 261 AA. Human PSA protein SEQ ID NO:78. WO2004022709-A2. IB-WAR-2004. (MANN-) MANNKIND CORP.
                                                                                                                                                                    ADC09580 standard; protein; 261 AA. PSA protein #SEQ ID 78. WO2003008537-A2.
                                                                                                                 34.2%;
40.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 34.2%;
Best Local Similarity 40.4%;
RESULT 1343
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Best Local Similarity 40.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 40.4%;
RESULT 1344
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PA (UYAR-) UNIV ARKANSAS.
Query Match
Best Local Similarity 40.
RESULT 1341
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AR-) UNIV ARKANS.

FY MATCh
Best Local Similarity 4
RESULT 1340
ID AD137157 stand?
DE Human prost
DE Human prost
PP 23-C
PA
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(GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-AUG-2000.
(COMP-) COMPUGEN LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-APR-2001.
(CORI-) CORIXA CORP.
                                                                                                                             Best Local Similarity RESULT 1337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                 Query Match
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RESULT 1345

ID AAB67545 standard; protein; 284 AA.

DE Amino acid sequence of protease MH2 catalytic domain in PPEK2-6XHIS-TAG.

PN W0200116289-A2.

PD 08-MAR-2001.

PA (ORTH) ORTHO-MCNEIL PHARM INC.

Query Match

Best Local Similarity 43.8%; Pred. No. 3.3e-28;

RESULT 1346
                                                                                                                                                                                                                                                                                                                  vuery Match 34.1%; Score 468.5; DB 7; Length 261; Beet Local Similarity 40.4%; Pred. No. 3.3e-28; RESULT 1347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 5; Length 231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 40.9%; Score 467; DB 1; Length 247; RESULT 1353

ID AAR82703 standard; protein; 247 AA.

DE Human pancreatic trypsin III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU74928 standard; protein; 312 AA.
Amino acid sequence of NS1-P703P mutated-His fusion protein.
WO200200867-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34.0%; Score 467; DB 2; Length 247; 40.9%; Pred. No. 4.1e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU74767 standard; protein; 312 AA.
Amino acid sequence of NS1-p703 mutated-His fusion protein.
0300200109109.A2.
03-JAM-2002.
(SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU74934 standard; protein; 231 AA.
Amino acid sequence of P703P mutated-His fusion protein.
WO200200867-A1.
                                                                                                                                                                                                                                                                                                                                                                                                        AAU74903 standard; protein; 231 AA.
Amino acid sequence of p703 mutated-His fusion protein.
WO200200708-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34.0%; Score 467.5; DB 4; 43.4%; Pred. No. 4.8e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34.0%; Score 467.5; DB 5; 43.4%; Pred. No. 4.8e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vuery Match 34.0%; Score 467.5; DB 5
Best Local Similarity 43.4%; Pred. No. 3.5e-28;
RESULT 1349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vuciy match 34.0%; Score 467.5; DB 5 Best Local Similarity 43.4%; Pred. No. 4.8e-28; RESULT 1352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAP81243 standard; protein; 247 AA.
Human spleen trypsin III (trysinogen III)
JP63160582-A.
                                                                                                                                                                                                                                       Human PSA precursor protein sequence. w02003047566-A2. 12-JUN-2003. (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY72521 standard; protein; 312 AA. NS1-P703P mutated-His fusion protein. W0200104143-A2. His Fusion protein. W0200104143-A2. SMITHLINE BEECHAM BIOLOGICALS. (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-JAN-2002.
(SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
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33.7%; Score 462.5; DB 8; Length 251; 40.2%; Pred. No. 9.3e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PD 16-JAN-1997.
PA (ORIN) ORION YHTYMAE OY.
Query Match 33.5%; Score 460.5; DB 2; Length 261;
Best Local Similarity 40.2%; Pred. No. 1.4e-27;
                                                                                                                                                                                                                                                                                                          33.7%; Score 462.5; DB 8; Length 251; 40.2%; Pred. No. 9.3e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1D ADP27545 standard; protein; 297 AA.

DE Human kallikrein-3 (KiK-3) EHT103 protien a variant SeqID 19.

DE HUMAN kallikrein-3 (KiK-3) EHT103 protien a variant SeqID 19.

PD 18-UNN-2004.

PA (EXON-) EXONHIT THERAPEUTICS SA.

QUERY MACCh

Bast Local Similarity 41.0%; Pred. No. 1.2e-27;

RESULT 1365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33.4%; Score 459.5; DB 5; Length 245; 41.4%; Pred. No. 1.5e-27;
                                                                                                                                                                                                                                                                                                          Query Match 33.7%; Score 462.5; DB 8; Length 251;
Best Local Similarity 40.2%; Pred. No. 9.3e-28;
RESULT 1363

ID ADP27546 standard; protein; 281 AA.

DE Human kallikrein-3 (KLK-3) EHT103 protien b variant SeqID 20.
PN FR2848569-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HOFF) ROCHE DIAGNOSTICS GMBH.

(HOFF) ROCHE DIAGNOSTICS GMBH.

33.4%; Score 459; DB 2; Length 238; ery Match

33.4%; Pred. No. 1.6e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 281;
                                                                                                                                232 #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 33.5%; Score 460.5; DB 2; Best Local Similarity 40.2%; Pred. No. 1.4e-27; RESULT 1366
                                                                                                     ADR66036 standard; protein; 251 AA,
Human prostatic carcinoma derived protein SEQ ID
WO2004076614-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                    18-JUN-2004.

(EXON-) EXONHIT THERAPEUTICS SA.

ery Match 33.6%; Score 462; DB 8;

ery Match 41.0%; Pred. No. 1.1e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU98921 standard, protein, 245 AA.
Human prostate specific antigen (PSA) variant.
WO200240059-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW10600 standard; protein; 261 AA.
Human prepro-Trp226-glandular kallikrein-2.
W09701630-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-MAY-2002.
(AMBI-) AMERICAN FOUND BIOLOGICAL RES INC.
(LOIK/) LOUKINOV D I.
(ZOUB/) ZOUBAK S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY08894 standard; protein; 238 AA.
Chimeric serine protease FXT protein.
EP927764-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR84668 standard; protein; 261 AA.
Prepro-hK2 kallikrein.
WO9530758-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB21314 standard; protein; 255 AA.
Human KLK2.
WO200053776-A2.
14-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-NOV-1995.
(MAYO-) MAYO FOUNDATION.
(HYBR-) HYBRITECH INC.
                                                                                                                                                                       10-SEP-2004.
(HINZ/) HINZWANN B.
(DAHL,) DAHL E.
(ROSE/) ROSENTHAL A.
(HERM/) HERMANN K.
(PILA/) PILARSKY C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PA (HOFF) ROCHE DIAGNO:
Query Match
Best Local Similarity
RESULT 1369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity RESULT 1368
                                                         Best Local Similarity
RESULT 1362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity RESULT 1364
(HERM/) HERMANN K. (PILA) PILARSKY C.
                                           Query Match.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADA50549 standard; protein; 237 AA.
Rhesus macaque prostate specific antigen (PSA/KLK3), SEQ ID NO:4.
WO2003031569-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      T2-JUN-2003.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
ery Match 33.8%; Score 464.5; DB 7; Length 261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-DEC-2003.

(ANTI-) ANTIGEN EXPRESS INC.

TY MATCH 33.7%; Score 463.5; DB 8; Length 261; Ft Local Similarity 40.0%; Pred. No. 8.1e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33.7%; Score 462.5; DB 8; Length 248; 40.2%; Pred. No. 9.2e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33.7%; Score 462.5; DB 8; Length 248; 40.2%; Pred. No. 9.2e-28;
                                                                                                                                Length 261;
                                                                                                                                                                                                                                                                                                                                   DB 5; Length 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 237;
                                                                                                                                                                                                                                                                                                                                                                                           ADJ59028 standard; protein; 261 AA.
Human PSA analogue (L155/Y154) precursor protein sequence.
WO2003047506-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADR66277 standard; protein; 248 AA.
Human prostatic carcinoma derived protein SEQ ID 131 #2.
WO2004076614-A2.
                    ADJ59026 standard; protein; 261 AA.
Human PSA analogue (Y154) precursor protein sequence.
WO2003047506-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADR66338 standard; protein; 248 AA.

Human prostatic carcinoma derived DNA SEQ ID 131 #4.

WO2004076614-A2.

(HINZ/) HINZMANN B.

(ROSE) ROSENTHAL B.

(ROSE) ROSENTHAL A.

(HERM/) PILARSKY C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADR66934 standard; protein; 251 AA.
Human prostatic carcinoma derived DNA SEQ ID 232 #4.
W02004076614-A2.
(HINZ/) HINZMANN B.
                                                       PD 12-JUN-2003.

RA (USSH ) US DEPT HEALTH & HUMAN SERVICES.

QUETY MATCH

Best Local Similarity 40.4%; Pred. No. 4.7e-28;

RESULT 1355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33.8%; Score 464; DB 6; 42.6%; Pred. No. 6.7e-28;
                                                                                                                                                                                       ABB84422 standard, peptide; 226 AA.
Rat SCCE protein N-terminal fragment SEQ ID 48.
W0200262135-A2.
15-AUC-2002.
(EGL/) EGELNUD T.
(HANS/) HANSSON L.
                                                                                                                                                                                                                                                                                                                               33.8%; Score 464.5; DB 5 42.7%; Pred. No. 5.8e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human prostate-specific antigen protein. 261 AA.
82002355594-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HINZ) HINZMANN B.
(DAHL/) DAHL B.
(ROSE) ROSENTHAL A.
(HERW/) HERMANN K.
(PILA/) PILARSKY C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-APR-2003.
(CENZ ) CENTOCOR INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
RESULT 1357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
RESULT 1360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (DAHL/) DAHL E.
(ROSE/) ROSENTHAL A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity RESULT 1361
                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity RESULT 1356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Si
RESULT 1358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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RESULT 1354
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BBBBB

PAPAPAPA

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PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match
33.4%; Score 458.5; DB 3; Length 255;
Best Local Similarity 40.8%; Pred. No. 1.9e-27;
RESULT 1370
                                                                                                                                                                                                                                                                                                                                   / Match 33.4%; Score 458.5; DB 2; Length 261; Local Similarity 40.8%; Pred. No. 2e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 33.4%; Score 458.5; DB 2; Length 261;
Best Local Similarity 40.8%; Pred. No. 2e-27;
RESULT 1374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A (MOUN) MOUNT SINAI HOSPITAL.

Query Match

Query Match

33.4%; Score 458.5; DB 3; Length 261;
                                                                                                                                                                                        Length 261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33.4%; Score 458.5; DB 2; Length 261; 40.8%; Pred. No. 2e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33.4%; Score 458.5; DB 7; Length 261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33.4%; Score 458.5; DB 4; Length 261; 40.8%; Pred. No. 2e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW45397 standard; protein; 261 AA.
Prostate-specific glandular kallikrein precursor prepro-hK2
WO9802748-A1.
                                                                                                                                                                                                                                     AAW83203 standard; protein; 261 AA.
Prostate-specific glandular kallikrein protein pphK2.
W09846795-A1.
                                                                                                                                                                           AAW06971 standard; protein; 261 AA.
Prostate-specific glandular kallikrein prepro-hK2
WO9634964-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 458.5; DB 2;
Pred. No. 2e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW96189 standard; protein; 261 AA.
Prepro human Kallikrein 2 (preprohK2).
WO9859073-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU06279 standard; protein; 261 AA.
Human Kallikrein2 polypeptide.
WO200145728-A2.
28-JUN-2001.
(EPIM-) EPIMMUNE INC.
                                                                                                                                                                                                                                                                                                                                                                               AAW49085 standard; protein; 261 AA.
Wild-type human Kallikrein 2 (hK2).
WO9821365-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADB75390 standard; protein; 261 AA. Prostate cancer marker protein. WO2003009814-A2. 06-FEB-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB21318 standard; protein; 261 AA
                                                                                                                                                                                                                                                                                 22-OCT-1998.
(BAYU ) BAYLOR COLLEGE MEDICINE.
(MAXO-) MAXO FOUNDATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MILL-) MILLENNIUM PHARM INC.
Query Match 33.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 33.4%;
Best Local Similarity 40.8%;
RESULT 1373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-DEC-1998.
(MAYO-) MAYO FOUNDATION.
(WOUN/) YOUNG C Y F.
(TIND/) TINDALL D J.
(KLEE/) KLEE G G.
                                                                                                                                   07-NOV-1996.
(HYBR-) HYBRITECH INC.
(MAYO-) MAYO FOUNDATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                     22-MAY-1998.
(MAYO-) MAYO FOUNDATION.
(HYBR-) HYBRITECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MAYO-) MAYO FOUNDATION. (HYBR-) HYBRITECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
RESULT 1377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity RESULT 1376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human KLK2.
WO200053776-A2.
                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                        Best Local
RESULT 1372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loca
RESULT 1375
                                                                                                                                                                                                                                        PPSSE
                                                                                                                                                                                                                                                                                                                                                                                          BBBBBB
                                                                                                      PA CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BBBBBBBB
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ID AAB19819 standard; protein; 237 AA.

DB Prostate specific antigen specific to benign prostatic hyperplasia.

PP WO200067030.A1.

PD 09-NOV-2000

PA (HYBR-) HYBRITECH INC.

PA (BAYU) BAYLOR COLLEGE MEDICINE.

Query Match

33.3%; Score 457.5; DB 4; Length 237;

Best Local Similarity 41.6%; Pred. No. 2.1e-27;

RESULT 1383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AABI9818 standard; protein; 237 AA.
Prostate specific antigen elevated in benign prostatic hyperplasia.
WO200066718-AI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 41.6%; Pred. No. 2.1e-27; RESULT 1384

ID ADASO546 standard; protein; 237 AA.

DE Human prostate specific antigen (PSA/KLK3), SEQ ID NO:1.

PD 17.8 no. 2.2.
                                                                                                                                                                                                                                                                                                                                              Query Match 33.3%; Score 457.5; DB 2; Length 237; Best Local Similarity 41.6%; Pred. No. 2.1e-27; RESULT 1380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 457.5; DB 6; Length 237; Pred. No. 2.1e-27;
                                                                                                                                                                                  Length 237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB11041 standard; peptide; 237 AA.
Human prostate-specific antigen N-terminal fragment #2.
EP1043394-A2.
                                                                DE Prostate-specific antigen protein hK3.
PN W09846795-A1.
PD 22-OCT-1999.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
PA (MAYO-) MAYO FOUNDATION.
33.3%; Score 457.5; DB 2;
Best Local Similarity 41.6%; Pred. No. 2.1e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PD 11-CT-2000.
PA (SERA.) SERATEC GES BIOTECHNOLOGIE MBH.
Query Match 33.3%; Score 457.5; DB 3;
BEST Local Similarity 41.6%; Pred. No. 2.1e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33.3%; Score 457.5; DB 6; 41.6%; Pred. No. 2.1e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33.3%; Score 457.5; DB 2 41.6%; Pred. No. 2.1e-27;
Best Local Similarity 40.8%; Pred. No. 2e-27; RESULT 1378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADA09840 standard; protein; 237 AA.
Human mature prostate specific antigen (PSA).
US2003059864-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                               AAW96187 standard; protein; 237 AA.
Human prostate specific antigen (FSA).
W09899073-A1.
30-DEC-1998.
(MAYO-) MAYO FOUNDATION.
(TIND/) TINDALL D J.
(KLEE/) KLEE G G.
                                                                                                                                                                                                                                                   AAW56086 standard; protein; 237 AA.
Human prostate specific antigen protein.
WO9810292-A1.
                                                     AAW83213 standard; protein; 237 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-NOV-2000.
(HYBR-) HYBRITECH INC.
(BAYU ) BAYLOR COLLEGE MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MIKO/) MIKOLAJCZYK S D. (RITT/) RITTENHOUSE H G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-APR-2003.
(CENZ ) CENTOCOR INC.
                                                                                                                                                                                                                                                                                                                      12-MAR-1998.
(CENZ ) CENTOCOR INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
RESULT 1385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity RESULT 1381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
RESULT 1386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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PD 25-WAR-2004.

PA (ANTI-) ANTIGEN EXPRESS INC.

Query Match 33.1%; Score 454.5; DB 8; Length 261;

Best Local Similarity 39.6%; Pred. No. 4e-27;

RESULT 1399
                                                                                                                                                                                                                                                                                                                PD 03-JAN-2002.

Query Match 33.1%; Score 454.5; DB 5; Length 232; Best Local Similarity 43.8%; Pred. No. 3.5e-27; RESULT 1397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 33.0%; Score 453.5; DB 7; Length 237; Best Local Similarity 41.6%; Pred. No. 4.3e-27; RESULT 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 32.9%; Score 452.5; DB 2; Length 244; Best Local Similarity 41.8%; Pred. No. 5.3e-27; RESULT 1402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32.9%; Score 452.5; DB 2; Length 244;
                                                                                                                                                                                                                  Length 232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 244;
                                                   33.1%; Score 454.5; DB 4; Length 232; 43.8%; Pred. No. 3.5e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW45396 standard; protein; 244 AA.
Prostate-specific glandular kallikrein precursor pro-hK2
WO9802748-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW83204 standard; protein; 244 AA.
Prostate-specific glandular kallikrein protein phK2.W09846795-A1.
(BAYU) BAYLOR COLLEGE MEDICINE.
(MAYO-) MAYO FOUNDATION.
                                                                                                                                                                                                                                                                   AAU74930 standard; protein; 232 AA.
Amino acid sequence of prostase protein fragment #1
WO200200867-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADJ59027 standard; protein; 237 AA.
Human PSA analogue (Y154) mature protein sequence.
WO2003047506-A2.
                                                                                                                                                                     Query Match 32.9%; Score 452.5; DB 2; Best Local Similarity 41.8%; Pred. No. 5.3e-27; RESULT 1401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 454.5; DB 2;
Pred. No. 3.7e-27;
                                                                                                    AAU74769 standard; protein; 232 AA.
Protein sequence of prostase homologue #1.
WQ200200708-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
PA (CORI-) CORIXA CORP. 33.1%; Score 454...
Best Local Similarity 43.8%; Pred. No. ...
RESULT 1395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR84669 standard; protein; 244 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW96188 standard; protein; 244 AA. Pro human Kallikrein 2 (prohK2). W09859073-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 33.1%;
Best Local Similarity 41.2%;
RESULT 1398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-JAN-1998.
(MAYO-) MAYO FOUNDATION.
(HYBR-) HYBRITECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MAYO-) MAYO FOUNDATION. (HYBR-) HYBRITECH INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (YOUN/) YOUNG C Y F.
(TIND/) TINDALL D J.
(KLEE/) KLEE G G.
                                                                                                                                                                                                           Query Match
Best Local Similarity
RESULT 1396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pro-hK2 kallikrein.
WO9530758-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 33.2%; Score 455.5; DB 2; Length 237; Best Local Similarity 41.6%; Pred. No. 3e-27; RESULT 1390
                                                                                                               DB 7; Length 237;
                                                                                                                                                                                                                                                                                    Query Match 33.3%; Score 457.5; DB 8; Length 237; Best Local Similarity 41.6%; Pred. No. 2.1e-27; RESULT 1388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 33.2%; Score 455.5; DB 2; Length 261; Best Local Similarity 40.8%; Pred. No. 3.3e-27; RESULT 1392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33.2%; Score 455.5; DB 2; Length 261; 40.8%; Pred. No. 3.3e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33.1%; Score 454.5; DB 2; Length 232; 43.8%; Pred. No. 3.5e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 237;
                                                                                                                                                                                                                                                                                                                                                                                                                            PA (BIOT-) BIOTECHN RES PARTN.
Query Match 33.2%; Score 456; DB 1; Length 245;
Best Local Similarity 39.7%; Pred. No. 2.9e-27;
RESULT 1389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Match 33.2%; Score 455.5; DB 7; Local Similarity 41.6%; Pred. No. 3e-27;
                                                                                                Query Match 33.3%; Score 457.5; DB 7; Best Local Similarity 41.6%; Pred. No. 2.1e-27; RESULT 1387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW45400 standard; protein; 261 AA.
Prostate-specific glandular kallikrein hK2v217.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW45398 standard, protein, 237 AA.
Prostate-specific antigen protein hK3 (PSA).
WO9802748-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW59129 standard; protein; 232 AA.
Homo sapiens Tub Interactor (hTI-1) protein.
WO9812302-A1.
                                Human PSA mature protein sequence.
20003047566-A2.
12-JUN-2003.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADUS9025 standard; protein; 237 AA. Human PSA mature protein sequence. Moo003047566-A2. 12-JUN-2003. (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                       ADF60980 standard; protein; 237 AA.
Human prostate specific antigen (PSA).
US2003166036-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW06972 standard; protein; 261 AA.
Kallikrein prepro-hK2v217 variant.
W09634964-A2.
                                                                                                                                                                                                                                                                                                                                                             AAP70677 standard; protein; 245 AA.
Human kallikrein gene product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY72523 standard; protein; 232 AA.
Human prostage antigen #1.
WO200104143-A2.
18-JAN-2001.
            ADJ59023 standard; protein; 237 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MILL-) MILLENNIUM PHARM INC.
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(MAYO-) MAYO FOUNDATION.
(HYBR-) HYBRITECH INC.
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(MAYO-) MAYO FOUNDATION.
(HYBR-) HYBRITECH INC.
                                                                                                                                                                                                                                     04-SEP-2003.
(MIKO/) MIKOLAJCZYK S D.
(RITT/) RITTENHOUSE H G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-NOV-1996.
(HYBR-) HYBRITECH INC.
(MAYO-) MAYO FOUNDATION
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Best Local Similarity
RESULT 1393
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                                                                                                                                                                                                                                                                                                                                                                                                      WO8702709-A.
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RESULT 1391
                                                                                                                                                                           BABABB
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WO2003031569-A2.
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PA (UYCO) UNIV COLUMBIA NEW YORK.
QUETY MATCh
BOST LOCAL Similarity 40.7%; Pred. No. 7.4e-27;
RESULT 1408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32.8%; Score 450.5; DB 2; Length 237; 42.0%; Pred. No. 7.4e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                18-JUN-2004.

(EXON-) EXONHIT THERAPEUTICS SA.

(EXY Match 32.9%; Score 452.5; DB 8; Length 297;

(ery Match 1.8%; Pred. No. 6.5e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 32.8%; Score 450.5; DB 2; Length 237; Best Local Similarity 42.0%; Pred. No. 7.46-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 32.8%; Score 450.5; DB 2; Length 237; Best Local Similarity 42.0%; Pred. No. 7.4e-27;
                                                                                                                                                               32.9%; Score 452.5; DB 2; Length 250; 40.5%; Pred. No. 5.4e-27;
                                                                                                                                                                                                                 ADP27538 standard; protein; 281 AA.
Human kallikrein-2 (KLK-2) EHT102 protein b variant SeqID 12.
PR2848569-A1.
                                                                                                                                                                                                                                                                                                                                                                             ADP27537 standard; protein; 297 AA.
Human kallikrein-2 (KLK-2) EHT102 protein a variant SeqID 11.
FR2848569-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 7; Length 236;
                                                                                                                                                                                                                                                                                                                               Length 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADJ59029 standard; protein; 236 AA.
Human PSA analogue (L155/Y154) mature protein sequence.
WO2003047506-A2.
12-JUN-2003.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
BY Match
SLOCAL Similarity 41.6%; Pred. No. 6.1e-27; Lengt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAM83202 standard; protein; 237 AA.
Prostate-specific glandular kallikrein protein hK2
WO9846795-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW45395 standard; protein; 237 AA.
Mature prostate-specific glandular kallikrein hK2.
WO9802748-A1.
                                                                                                                                                                                                                                                                                                                               8
Best Local Similarity 41.8%; Pred. No. 5.3e-27;
RESULT 1403
                                                                                                                                                                                                                                                                              I8-JUN-2004.

(EXON-) EXONHIT THERAPEUTICS SA.

(EXON-) EXONHIT THERAPEUTICS SA.

32.9%; Score 452.5; DB 8

Query Match

32.9%; Score 452.5; DB 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -AAT77098 standard; protein; 237 AA. Prostate-specific antigen. WO9528498-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 1410
ID AAW96186 standard, protein, 237 AA.
DE Mature human Kallikrein 2 (hK2).
                                                          AAW03130 standard; protein; 250 AA.
Prostate-specific antigen.
W09621042-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADASO561 standard; protein; 237 AA.
Kallikrein KLK2, SEQ ID NO:16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-OCT-1998.
(BAYU ) BAYLOR COLLEGE MEDICINE.
(MAYO-) MAYO FOUNDATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-JAN-1998.
(MAYO-) MAYO FOUNDATION.
(HYBR-) HYBRITECH INC.
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(YOUN/) YOUNG C Y F.
(TIND/) TINDALL D J.
(KLEE/) KLEE G G.
                                                                                                                                                           Query Match
Best Local Similarity
RESULT 1404
                                                                                                                    11-JUL-1996.
(UYBO-) UNIV BOSTON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
RESULT 1406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
RESULT 1405
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30-DEC-1998.
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ADJ83076 standard; protein; 217 AA.
Trypsin protein which is related to human NOVX protein - SEQ ID 67.
US2003170630-A1.
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                        Length 237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 217;
                                                                                                                                                                                                                                                                                                Length 237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 217;
                                                                                                                                                                                                                                                                                                                                                              Polypeptide homologous to a human NOVX domain SeqID 813. WO20026849-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADI17269 standard; protein; 217 AA.
Polypeptide homologous to a human NOVX domain SeqID 805.
WO200268649-A2.
                                                                                                                                                                                                                                                                                                                                                                                       vuery Match
Best Local Similarity 44.4%; Score 447.5; DB 5;
RESULT 1414
ID AD17259 standard; protein; 217 AA.
DB Polypeptide homologous to a by WC200268649-A2.
PA WC200268649-A2.
PA //www.pa wc. 2002 w control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the
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                           DB 6;
                                                                                                                                                                                                                                                                                             Score 448.5; DB 2;
Pred. No. 1e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 447.5; DB 7;
Pred. No. 1.1e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 5;
                           Score 450.5; DB 6;
Pred. No. 7.4e-27;
                                                                                                            AAR84667 standard; protein; 237 AA.
Mature kallikrein hK2.
WO9530758-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW83212 standard; protein; 237 AA.
hK2 variant A217V.
WO9846795-A1.
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(BAYU ) BAYLOR COLLEGE MEDICINE.
(MAYO-) MAYO FOUNDATION.
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44.4%;
                                                                                                                                                                                                                                                                                                                   Best Local Similarity 42.0%;
RESULT 1413
ID AD117277 standard; protein;
                           32.8%;
                                                                                                                                                                                                                                                                                             32.6%;
                                                          42.08;
                                                                                                                                                                                                                                  (MAYO-) MAYO FOUNDATION. (HYBR-) HYBRITECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALSOBROOK J P.
TCHERNEV V T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIU X.
SPYTEK K A.
ZERHUSEN B D.
PATTURAJAN M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SHIMKETS R A. GROSSE W M. SZEKERES E S. VERNET C A M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FERNANDES E R.
RIEGER D K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EDINGER S. R. GUNTHER B. MILLET I. SCIORE P. ELLERMAN K. MACDOUGALL J.
(CENZ ) CENTOCOR INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GANGOLLI E A
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BURGESS C E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CASMAN S J. BOLDOG F L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity RESULT 1416
                                                 Best Local Similarity RESULT 1412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMITHSON G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity RESULT 1417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GORMAN L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .1-SEP-2003
                                                                                                                                                                                                                                                                                                Query Match
                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TCHE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ALSO/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ELLE/)
(MACD/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SMIT/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CASM/
(BOLD/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SCIO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZERH/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GUNTY/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PATT/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VERN/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GORM/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (EDIN/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MILLL/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BURG/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SHIM/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GANG/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FERN/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RIEG/
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Length 205;

Length 227;

Length 205;

Length 205;

Length 205

Length 205;

- 44 - 44

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Prostate tumour antigen predicted amino acid sequence for P703P-DE13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW71872 standard; protein; 205 AA.
Protein encoded by prostate tumour clone P703 splice variant DE13.
WO9837093-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY82005 standard; protein; 205 AA.
Human immunogenic prostate tumour protein sequence SEQ ID NO:176
WO200004149-A2.
                                                                                                                                                                                                                                                                   ADE70966 standard; protein; 227 AA.
Human protein modification and maintenance molecule (PMMM)-4.
WO2003063688-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31.0%; Score 426.5; DB 4; Length 205; 43.7%; Pred. No. 4.5e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31.0%; Score 426.5; DB 2; Length 205; 43.7%; Pred. No. 4.5e-25;
                30-MAR-1998.
(MOKA-) MOKAM BIOTECHNOLOGY RES INST.
ery Match
31.7%; Score 436; DB 2; Length 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABG94414 standard; protein; 205 AA.
Human prostate tumour protein partial variant sequence :
US2002090372-A1.
                                                                                                          AAB50447 standard, protein, 205 AA.
Human prostate cancer-related intracellular protein #1.
WO200071711-A2.
30-MO2000 (SAAIT), SAAITCIOGLU F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aumiu1120 standard; protein; 205 AA.
Human prostate-specific amino acid sequence P703P-DE13.
W0200151633-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 426.5; DB 4;
Pred. No. 4.5e-25;
                                                                                                                                                                                                 vuery Match
31.4%; Score 431.5; DB 4;
Best Local Similarity 44.2%; Pred. No. 1.8e-25;
RESULT 1427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31.0%; Score 426.5; DB 3; 43.7%; Pred. No. 4.5e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                          AAW69388 standard; protein; 205 AA.
Prostate tumour specific gene clone DE13 protein.
WO9837418-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 426.5; DB 2;
Pred. No. 4.5e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31.0%; Score 426.5; DB 3; 43.7%; Pred. No. 4.5e-25;
                                                                                                                                                                                                                                                                                                                              PD 07-AUG-2003.

PA (INCY-) INCYTE GENOMICS INC.

Query Match 31.3%; Score 430; DB 7;

Best Local Similarity 39.2%; Pred. No. 2.7e-25;

RESULT 1428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU69766 standard, protein; 205 AA.
Human prostate cDNA encoded protein #6.
WO200173032-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB74803 standard; protein; 205 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-AUG-1998.
(CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-JUL-2001.
(CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-OCT-2001.
(CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-AUG-1998.
(CORI-) CORIXA CORP.
                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity RESULT 1433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity RESULT 1430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (DILL/) DILLON D C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
RESULT 1432
ID AAMO1120 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
RESULT 1429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
RESULT 1431
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  KR98002267-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-JAN-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAM52944 standard; protein; 260 AA.
Agkistrodon halys brevicaudus thrombin-likle protease, salmobin.
                                                                                                                  Length 237;
                                                                                                                                                                                                                                                                                                                                32.6%; Score 447.5; DB 2; Length 237; 42.0%; Pred. No. 1.3e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 436.5; DB 4; Length 233; Pred. No. 8.7e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 237,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vuery Match 32.2%; Score 443; DB 8; Length 227;
Best Local Similarity 39.6%; Pred. No. 2.7e-26;
RESULT 1422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABM82643 standard; protein; 227 AA.
Human diagnostic and therapeutic pprotein SEQ ID NO:2892.
WO2004023973-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR94526 standard; protein; 279 AA.
Korean Viper Salmosa thrombin-like protease, Halybin.
EP707067-A2.
                                                                                                              Query Match 32.6%; Score 447.5; DB 2;
Best Local Similarity 42.0%; Pred. No. 1.3e-26;
RESULT 1418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32.4%; Score 444.5; DB 2; 41.1%; Pred. No. 2.1e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-APR-1996.
(MOGA-) MOGAM BIOTECHNOLOGY RES INST.
ery Match 32.0%; Score 439; DB 2;
ery Match 37.7%; Pred. No. 6.7e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 32.1%; Score 441.5; DB 2 Local Similarity 40.9%; Pred. No. 3.6e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 445; DB 2
Pred. No. 2e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mamushi fibrinolytic enzyme, brevinase. KR2001045716-A. Con-Un-2001.
AAW49087 standard, protein, 237 AA.
Mutant human Kallikrein 2 (hK2) A217V.
WO9821365-A2.
                                                                                                                                                                     AAW96190 standard; protein; 237 AA. Variant human Kallikrein 2 (hK2). W09859073-A1.
                                                                                                                                                                                                                                                                                                                                                                                    AAW11023 standard; protein; 240 AA.
Human prostate specific antigen.
WO9640754-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR84670 standard, protein; 238 AA.
Mature kallikrein hK2.
WO9530758-Al.
16-NOV-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR84671 standard; protein; 237 AA.
Mature kallikrein hK3.
WO9530758-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    y Match 32.4%;
Local Similarity 41.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                              19-DEC-1996.
(TEXA ) UNIV TEXAS SYSTEM.
                                                    22-MAY-1998.
(MAYO-) MAYO FOUNDATION.
(HYBR-) HYBRITECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-NOV-1995.
(MAYO-) MAYO FOUNDATION.
(HYBR-) HYBRITECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MAYO-) MAYO FOUNDATION. (HYBR-) HYBRITECH INC.
                                                                                                                                                                                                                                               (MAYO-) MAYO FOUNDATION.
(YOUN/) YOUNG C Y F.
(TIND/) TINDALL D J.
(KLEE/) KLEE G G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , MAYO FOUNDA.
-dR-) HYBRITECH IN
Best Local Similarity 4.
RESULT 1421
ID ABM82643 standar
DE Human diagr.
PN WO200400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-MAR-2004.
(INCY-) INCYTE CORP.
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity RESULT 1424
                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (LEEJ/) LEE J W. (PARK/) PARK W.
                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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RESULT 1420
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RESULT 1423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 1425
  222244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PARAGE
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Query
                                                                                                               Score 426.5; DB 4; Length 205;
Pred. No. 4.5e-25;
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                              Length 205;
                                                                                                                                                                                                                                                                                                                                                                                                                   Score 426.5; DB 4; Length 205;
Pred. No. 4.5e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 205;
                                                          AAG99005 standard; protein; 205 AA.
Human prostate-specific amino acid sequence P703P-DE13
WO200134802-A2.
                              DB 4;
                              31.0%; Score 426.5; DB 4 43.7%; Pred. No. 4.5e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31.0%; Score 426.5; DB 4; 43.7%; Pred. No. 4.5e-25;
                                                                                                                                            ABU71656 standard; protein; 205 AA.
Prostate cancer specific antigen P703P #2.
US2002192763-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB95225 standard; protein; 205 AA.
Human P703P-DE13 protein SEQ ID NO 176.
US2002022248-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human prostate tumour protein DE13.
US6262245-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU04964 standard; protein; 205 AA.
                                                                                                               31.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                   31.0%;
                                                                                                                                                                                                                                                                                                                      WANG A...
SKEIKY Y A W...
HEPLER W T...
HENDERSON R A...
HURAL J...
MCNEILL P D...
HOUGHTON R L...
Y DE BASSOLS C V...
                                                                                                                                                                                               DILLON D C.
MITCHAM J L.
HARLOCKER S L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LISX.
WANGA.
SKEIKYYAW.
HEPLERWT.
HENDERSONRA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MITCHAM J L.
HARLOCKER S L.
                                                                                          17-MAY-2001.
(CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-JUL-2001.
(CORI-) CORIXA CORP.
                   (CORI-) CORIXA CORP.
                                                                                                            Query Match
Best Local Similarity
RESULT 1436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                          VEDVICK T S.
CARTER D.
                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                    Best Local Similarity RESULT 1435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FANGER G R. RETTER M W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DILLON D C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STOLK J A.
DAY C H.
VEDVICK T S
CARTER D.
                                                                                                                                                                                                                             JIANG Y. KALOS M D.
                                                                                                                                                                                                                                                   FANGER G R.
RETTER M W.
                                                                                                                                                                                                                                                                      STOLK J A.
DAY C H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KALOS M D.
WO200125272-A2.
           12-APR-200
                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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(HEPL/)
(HEND/)
                                                                                                                                                                                                                                                                                                                                                                                                (DBAS/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HARL/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JIAN/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FANG/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WANG/
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ABB09589 standard; protein; 234 AA.
Deinagkistrodon acutus venom thrombin-like protein (234 residue variant).
CN1181421-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABU92024 standard; protein; 218 AA.
Human protein modification and maintenance molecule-4 (PMMM-4).
WO2003031939-A2.
                                                                                                                                                             Length 205;
                                                                                                                                                                                                                                                                                                                         DB 6; Length 205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADEIS982 standard, protein, 218 AA.
G-coupled protein receptor related polypeptide, SEQ ID No 12.
W0200283841.A2.
24-0CT-2002.
(CURA-) CURAGEN CORP.
30.6%; Score 420; DB 7; Length 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 205;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 225;
                                                                                                                                                                                                                    ABRE4337 standard; protein; 205 AA.
Prostate tumour specific protein sequence SEQ ID 176.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 MAY-1998.
(SHAN-) SHANGHAI BIO-CHEM INST CHINESE ACAD SCI.
ery Match
at Local Similarity 36.4%; Pred. No. 1e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 7;
Best Local Similarity 43.7%; Pred. No. 4.5e-25; RESULT 1439
                                                                                                                                                             Score 426.5; DB 5 Pred. No. 4.5e-25;
                                                                                                                                                                                                                                                                                                                     31.0%; Score 426.5; DB 6 43.7%; Pred. No. 4.5e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31.0%; Score 426.5; DB 7 43.7%; Pred. No. 4.5e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLOUS 17-APR-2003.
17-APR-2003.
(INCY-) INCYTE GENOMICS INC.
30.7%; Score 422; DB 6; ery Match 37.8%; Pred. No. 1.1e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-DEC-2000.
(BJRK) BJARNASON J B.
16ry Match 30.6%; Score 421; DB 4;
1ery Match 44.3%; Pred. No. 1.38-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 422.5; DB 5
Pred. No. 1.3e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31.0%; Score 426.5; DB 743.7%; Pred. No. 4.5e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB31579 standard, peptide; 225 AA.
Amino acid sequence of cod trypsin isozymes.
WO200078332-A2.
                                                                                                                                                                                                                                                                                                                               Best Local Similarity 43.7%; Pred. No. 4.5e RESULT 1441

1D ADB1956s etandard; protein; 205 AA.

DE Human prostate specific protein P703P-DE13.

PN US2003185830-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human prostate-specific polypeptide #6.
US2003157089-A1.
                                    ABG76668 standard; protein; 205 AA. Prostate tumour protein #6. US2002081580-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADG26042 standard; protein; 205 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADK36957 standard; protein; 281 AA.
Novel human polypeptide SeqID9039.
WO200216439-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30.7%;
                                                                                                                                                             31.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PD 21-AUG-2003.
PA (CORI-) CORIXA CORP.
Query Match
Best Local Similarity 4
RESULT 1443
                                                                                                                                                                                                                                                                              14-NOV-2002.
(CORI-) CORIXA CORP.
                                                                                                                      (DILL/) DILLON D C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CORI-) CORIXA CORP.
                                                                                                                                                           Query Match
Best Local Similarity
RESULT 1440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
RESULT 1447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
RESULT 1442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity RESULT 1444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
RESULT 1446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2002.
(HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                             WO200289747-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                             02-OCT-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 1445
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ADG75684 standard; protein; 215 AA.
Human protein modification and maintenance molecule polypeptide SegIDB.
WO2003083084-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 412.5; DB 8; Length 198;
Pred. No. 5.2e-24;
 Score 412.5; DB 6; Length 198;
Pred. No. 5.2e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 29.8%; Score 409; DB 6; Length 194;
Best Local Similarity 38.7%; Pred. No. 9.5e-24;
RESULT 1456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29.8%; Score 409; DB 7; Length 215; 37.1%; Pred. No. 1.1e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABM62829 standard; protein; 215 AA.

Human diagnostic and therapeutic pprotein SEQ ID NO:3078.

W W2004022973-A2.

25-MAR-2004.

A (INCY-) INCYTE CORP.

29.8%; Score 409; DB 8; Length 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABM83248 standard; protein; 299 AA.
Human diagnostic and therapeutic pprotein SEQ ID NO:3497.
WO2004023973-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 36.8%; Pred. No. 5.2e-24;
RESULT 4455
DE Prostate specific antigen (PSA/KLK3), SEQ ID No:15.
PN W02003031569-A2.
PD T7-ARE-2003.
PA (CENZ ) CENTOCOR INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29.8%; Score 409; DB 8; 37.1%; Pred. No. 1.1e-23;
                                                ADN62900 standard; protein; 198 AA.
 30.0%;
36.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STONE D J.
STONE D J.
SHENOY S G.
SHINKETS R A.
ROTHENBERG M E.
LEACH M D.
AGEE M L.
BERGHS C.
DIPIPPO V A.
EISEN A.
                                                                                                                                                                                                                                                                                                                     ORT T.
GORMAN L.
ZERHUSEN B D.
ANDERSON D W.
ZHONG M.
CATTERTON E.
                                                                                                                                                                                                                                                                                                     MALYANKAR U M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RIEGER D K.
SPADERNA S K.
                                                                                                                                                                                                                                     PATTURAJAN M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0 09-OCT-2003.
(INCY-) INCYTE CORP.
Query Match
                                                                                                                                                                                                                                                                   EDINGER S R.
ELLERMAN K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity RESULT 1457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity RESULT 1458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAR-2004.
(INCY-) INCYTE CORP.
                                                                                                                                    MILLET I.
PEYMAN J A.
KEKUDA R.
               Best Local Similarity RESULT 1454
                                                                                                                  SMITHSON G.
                                                                                                                                                                                                                                                        SPYTEK K A.
                                                                                                                                                                                                                                                                                                                                                                                                                                      MILLER C E. RASTELLI L.
                                                                                 US2004038223-A1.
26-FEB-2004.
                                                                   Human NOV18c
   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (EISE/)
(GANG/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SPAD/)
                                                                                                                                     (MILL/)
(PEYM/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (RIEG/)
                                                                                                                                                                   (KEKU/)
                                                                                                                                                                                                                                                                                                                       (ORTT/)
(GORM/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BERG/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SHEN/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SHIM/
                                                                                                                                                                                                                                                                                                                                                        (ZERH/
                                                                                                                                                                                                                                                                                                                                                                         ANDE/
                                                                                                                                                                                                                                                                                                                                                                                                       CATT/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (STON/
                                                                                                                                                                                                                                                                                                       MALY/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30.3%; Score 416.5; DB 6; Length 226; 42.6%; Pred. No. 2.9e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 218;
                                 ADL93921 standard; protein; 218 AA.
Human G-coupled protein receptor-related protein #6.
US2004006205-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04.APR-2002.
(MILL-) MILLENNIUM PHARM INC.
(MILL-) MILLENNIUM PHARM INC.
30.3%; Score 416.5; DB 5;
ery Match
42.6%; Pred. No. 2.9e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-406-1999.
(HUMA-) HUMAN GENOME SCI INC.
30.4%; Score 418; DB 2;
ery Match
frimilarity 46.1%; Pred. No. 2e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 420; DB 8;
Pred. No. 1.5e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30.4%; Score 417.5; DB 2 36.6%; Pred. No. 2.5e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY28641 standard; protein; 207 AA.
Human secreted protein from cDNA clone HKAET41.
WO9940183-A1.
   37.8%; Pred. No. 1.5e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE21442 standard; protein; 226 AA.
Human trypsin domain consensus protein #2.
WO200226802-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Trypsin domain consensus sequence, SMART.
US2002165152-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-DEC-1997.
A (MOGA-) MOGAM BIOTECHNOLOGY RES INST.
Query Match
30.4%; Score 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW46773 standard; protein; 233 AA. Amino acid sequence of Salmonase. EP814164-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 42.6%; Pred. 1
RESULT 1452
ID ABG75786 standard; protein; 226 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADAO5736 standard; protein; 198 AA.
Human NOV18c protein SEQ ID NO:96.
WQ2003029424-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (KAPE/) KAPELLER-LIBERMANN R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30.6%;
37.8%;
                                                                                                                                                                                                                                                                   CASMAN S J.
BOLDOG F L.
VOSS E Z.
VERNET C A.
MACDOUGALL J R.
RASTELLI L.
ANDERSON D W.
                                                                                                                                                                                                                                                                                                                                                                                                                     FURTAK K.
PATTURAJAN M.
BURGESS C E.
MALYANKAR U M.
SHIMKETS R A.
TAUPIER R J.
                                                                                                           GERLACH V.
LIU X.
MILLER C E.
SPYTER K A.
ZERHUSEN B D.
PENA C E A.
SHENOY S G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-APR-2003.
(CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
RESULT 1450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity RESULT 1451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
Best Local Similarity RESULT 1448
                                                                                                                                                                                                                                                                                                                                                                                     ZHONG M.
MEZES P S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                     ZHONG H.
SMITHSON G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MAZU/) MAZUR A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Si
RESULT 1449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                 (GERL/)
(LIUX/)
(MILL/)
(SPYT/)
                                                                                                                                                                                                    PENA/)
                                                                                                                                                                                                                       (SHEN/)
                                                                                                                                                                                                                                                                                                       (\ssox
                                                                                                                                                                                                                                                                                                                                                      RAST/)
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29.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Batroxobin gene product. JP02124092-A.
                                                                                                                                                                25-MAR-2004.
(INCY-) INCYTE CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                      JP63049084-A.
01-MAR-1988.
(YAMA/) YAMASHINA I.
 Query Match
Best Local Similarity
RESULT 1464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Araraca batroxobin.
WO9929838-A1.
                                                                                                                                                                                                Best Local Similarity
RESULT 1466
                                                                                                                                                                                                                                                                                            Best Local Similarity RESULT 1467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
RESULT 1469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
RESULT 1470
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                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity RESULT 1468
                                                                                                                                                                                                                                                                                                                                                                   (BADI ) BASF AG.
                                                                                                                                                                                                                                                                                                                                             DE4023699-A.
                                                                                                                                                                                                                                                                                                                                                         30-JAN-199
                                                                                                                                                                                                                                                                                                                                                                                                                             Batroxobin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                          Ouery Match
                                                                                                                                                                                                                                                                                   Query Match
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                                                                                             Length 181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29.6%; Score 406.5; DB 3; Length 230; 36.2%; Pred. No. 1.8e-23;
   Length 299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABM82641 standard; protein; 222 AA.
Human diagnostic and therapeutic pprotein SEQ ID NO:2890.
WO2004023973-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW76538 standard; protein; 231 AA.
A. contortrix protein C activator protein fragment.
WO9842850-A1.
                                                                                             Score 408.5; DB 6;
Pred. No. 9.6e-24;
 Score 409; DB 8;
Pred. No. 1.5e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 408.5; DB 8, Pred. No. 9.6e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29.6%; Score 407; DB 8; 36.7%; Pred. No. 1.6e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB08510 standard; protein; 230 AA.
A recombinant protein C activator polypeptide.
                                  ADA05738 standard; protein; 181 AA.
Human NOV18d protein SEQ ID NO:98.
WO2003029424-A2.
                                                                                                                               ADN62902 standard; protein; 181 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29.7%;
37.4%;
  29.8%;
38.6%;
                                                                                             29.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (INLI) INSTRUMENTATION LAB. Query Match 29.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (RPMS-) RPMS TECHNOLOGY LTD
                                                                                                                                                                                                                                                                                                                                                                                                                         STONE D J.
PENA C E A.
SHENOY S G.
SHIMKETS R A.
ROTHENBERG M E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGEE M L.
BERGHS C.
DIPIPPO V A.
EISEN A.
GANGOLLI E A.
                                                                                                                                                                                                                                                                                                         MALYANKAR U M.
                                                                                                                                                                                                                                                                                                                              GORMAN L.
ZERHUSEN B D.
ANDERSON D W.
                                                                     10-APR-2003.
(CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                 GUO X.
PATTURAJAN M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RIEGER D K.
SPADERNA S K.
Query Match
Best Local Similarity
RESULT 1459
ID ADA05738 standard, pr
DE Human NOV18d protein
PN W02003029424-A2.
PD 10-ARR-2003.
PA (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                  EDINGER S R.
ELLERMAN K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-MAR-2004.
(INCY-) INCYTE CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                            CATTERTON E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity RESULT 1462
                                                                                                                                                                                                   PEYMAN J A. KEKUDA R.
                                                                                                                                                                            SMITHSON G.
                                                                                                                                                                                                                                                                         SPYTEK K A.
                                                                                                                                                                                                                                                                                                                                                                                                     MILLER C E.
RASTELLI L.
                                                                                                      Best Local Similarity
RESULT 1460
                                                                                                                                                      JS2004038223-A1.
                                                                                                                                                                                                                                                                                                                                                                    ZHONG M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200050612-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SPAD/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (RIEG/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (EISE/
                                                                                              Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best 1
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ABB09590 standard; protein; 218 AA.
Deinagkistrodon acutus venom thrombin-like protein (218 residue variant).
CN1181421-A.
Length 231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 5; Length 249;
                                                                                                                                                            Length 218,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AMSOCOLLO
30-MAR-1998.
(MOKA-) MOKAM BIOTECHNOLOGY RES INST.
29.1%; Score 400; DB 2; Length 231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 255;
                                                                                                                                                                                                                                                                                                                               Length 220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 255;
                                                                                                                                                                                                                       ABM84665 standard; protein; 220 AA.
Human diagnostic and therapeutic pprotein SEQ ID NO:4914.
WO2004023973-A2.
                                                                                                                                                                                                                                                                                                                                                                                    AABO8511 standard; protein; 230 AA.
Blosynthetic variant of protein C activator polypeptide.
W0200050612-A2.
31-AUG-2000.
(INLI ) INSTRUMENTATION LAB.
    5;
                                                                                                           PD 13-WAY-1998.

PA (SHAN-) SHANGHAI BIO-CHEM INST CHINESE ACAD SCI.

QUECY MATCh

29.5%; SCORE 405.5; DB 5;

BUST LOCAL SIMILATITY 36.5%; Pred. No. 2e-23;

RESULT 1465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3,
Score 406.5; DB 2
Pred. No. 1.8e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29.2%; Score 401.5; DB 5, 40.3%; Pred. No. 4.6e-23;
                                                                                                                                                                                                                                                                                                                             29.5%; Score 405; DB 8; 36.7%; Pred. No. 2.2e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 402; DB 1;
Pred. No. 4.3e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29.3%; Score 402; DB 2; 32.9%; Pred. No. 4.3e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Beet Local Similarity 32.9%; Pred. No. 4.3e-23; RESULT 1471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 403; DB 2;
Pred. No. 3.3e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 403.5; DB
Pred. No. 3e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR20557 standard; protein; 234 AA.
Fibrinogenolytic protein #4 from snake venom.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAE21441 standard; protein; 249 AA.
Human trypsin domain consensus protein #1.
WO200226802-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAM52946 standard; protein; 231 AA.
Batroxobin, a snake venom protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAP81333 standard; protein; 255 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR05436 standard; protein; 255 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY17869 standard; protein; 255 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-JUN-1999.
(BRIM ) BRISTOL-MYERS SQUIBB CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-MAY-1990.
(FUJI ) FUJISAWA PHARM CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-APR-2002.
(MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29.3%;
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Query
                             AABII711 standard; protein; 264 AA.
Mouse serine protease BSSP5 (mBSSP5) SEQ ID NO:4.
W0200031243-A1.
02-JUN-2000.
(FUSO ) FUSO PHARM IND LTD.
ery Match
st Local Similarity 39:1%; Pred. No. 1.4e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28.5%; Score 391; DB 7; Length 253; 38.0%; Pred. No. 3e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 389; DB 7; Length 253; Pred. No. 4.3e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28.2%; Score 388; DB 1; Length 269; 38.5%; Pred. No. 5.5e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28.2%; Score 387; DB 7; Length 253;
                                                                                                                                                                                                                                                                  Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                              Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABM82831 standard; protein; 233 AA.
Human diagnostic and therapeutic pprotein SEQ ID NO:3080.
WO2004023973-A2.
25-WAR-2004.
(INCY-) INCYTE CORP.
                                                                                                                                                                                                                                                              Score 394; DB 2;
Pred. No. 1.7e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Trypsin domain consensus sequence, PFAM.
US2002165152-A1.
O7-NOV-2002.
(KAPE), KAPELLER-LIBERMANN R.
28.3%; Score 389; DB 6;
ery Match
21.10cal Similarity 40.4%; Pred. No. 3.9e-22;
                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28.5%; Score 392; DB 8; 36.8%; Pred. No. 2.3e-22;
34.2%; Pred. No. 5.6e-23;
                                                                                                                                                                                                                                                                                                   AAR20556 standard; protein; 236 AA.
Fibrinogenolytic protein #3 from snake venom.
DE4023699-A.
                                                                                                                                                                                                                                                                                                                                                                                                          28.6%; Score 393; DB 2 37.3%; Pred. No. 2e-22;
                                                                                                                                                                                                                                              (MOKA-) MOKAM BIOTECHNOLOGY RES INST.
28.7%; Score 39
st Local Similarity 36.8%; Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADE58223 standard; protein; 253 AA.
Human Protein P00746, SEQ ID NO 4094.
WO2003016475-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human adipsin protein; 253 AA. US2003092620-A1.
                                                                                                                                                                           AAM52945 standard; protein; 236 AA.
Plaboxobin, a snake venom protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE39992 standard, protein; 253 AA. Human adipsin protein #1. US2003092620-A1. 15-MAY-2003. (GEST ) GENSET SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAP70758 standard; protein; 269 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABG75785 standard; protein; 227 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28.3%;
38.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-FEB-2003.
(GEHO ) GEN HOSPITAL CORP.
(FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pig pancreas elastase-2. JP62000276-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-JAN-1987.
(SANY ) SANKYO CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
RESULT 1479
Best Local Similarity
                                                                                                                                   Best Local Similarity RESULT 1474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity
RESULT 1478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity RESULT 1481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-MAY-2003.
(GEST ) GENSET SA.
                                                                                                                                                                                                                                                                                                                                                                                      PA (BADI ) BASP AG.
Query Match
Best Local Similarit
RESULT 1476
                                                                                                                                                                                                          KR98002267-A.
                                                                                                                                                                                                                                                                                                                                                                         30-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Si
RESULT 1477
                                                                                                                                                                                                                                                              Query Match
Best Local Si
RESULT 1475
                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                      A D A G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A D M E D
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DE Tumour-associated antigenic target (TAT) polypeptide PRO2719, SEQ:4580. PN WO2004030615-A2. PD 15-APR-2004. PN GETH ) GENENTECH INC. 28.1%; Score 385.5; DB 8; Length 264; Best Local Similarity 36.8%; Pred. No. 8.4e-22;
                                                                                                            PD 02-JUN-2000.

PA (FUSO ) FUSO PHARM IND LTD.

Query Match 28.1%; Score 386.5; DB 3; Length 264;

Best Local Similarity 36.8%; Pred. No. 7e-22;

RESULT 1483
                                                                                                                                                                                                                                                                                                                      28.1%; Score 386.5; DB 6; Length 264; 36.8%; Pred. No. 7e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28.0%; Score 385; DB 8; Length 213; 40.2%; Pred. No. 7.4e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABM82644 standard; protein; 212 AA.
Human diagnostic and therapeutic pprotein SEQ ID NO:2893.
WO2004023973-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABM82830 standard; protein; 212 AA.
Human diagnostic and therapeutic pprotein SEQ ID NO:3079-
WO2004023973-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADR66037 standard; protein; 213 AA.
Human prostatic carcinoma derived protein SEQ ID 233 #1.
WO2004076614-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADR66935 standard; protein; 213 AA.
Human prostatic carcinoma derived DNA SEQ ID 233 #4
WO2004076614-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 36.3%; Pred. No. 6.7e-22;
RESULT 1487
                                    AAB11710 standard; protein; 264 AA.
Human serine protease BSSP5 (hBSSP5) SEQ ID NO:2.
WO200031243-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28.1%; Score 385.5; DB 8; 36.3%; Pred. No. 6.7e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                       MC2002-17-AD03.
17-AD03.
(MILL-) MILLENNIUM PHARM INC.
28.1%; Score 386; DB 6;
ery Match
28.1%; Pred. No. 7.9e-22;
Best Local Similarity 38.5%; Pred. No. 6.2e-22; RESULT 1482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 385; DB 8;
Pred. No. 7.4e-22;
                                                                                                                                                                                                                ABR39439 standard; protein; 264 AA.
Human GENSET polypeptide clone name vCTRL-1.
20-FEB-2003.
                                                                                                                                                                                                                                                                                                                                                                                ABU00382 standard; protein; 271 AA.
Consensus sequence of trypsin-like domain.
WO2003031463-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28.0%;
40.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
RESULT 1485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-MAR-2004.
(INCY-) INCYTE CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-MAR-2004.
(INCY-) INCYTE CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
RESULT 1486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (DAHL/) DAHL E.
(ROSE/) ROSENTHAL A.
(HERM/) HERMANN K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DAHL E.
ROSENTHAL A.
                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
RESULT 1484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-SEP-2004.
(HINZ/) HINZMANN B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PILA/) PILARSKY C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HERM/) HERMANN K.
(PILA/) PILARSKY C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                    (GEST ) GENSET SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-SEP-2004
                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match
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PD 21-FEB-2002.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 27.8%; Score 382.5; DB 5; Length 171;
Best Local Similarity 35.8%; Pred. No. 9.2e-22;
RESULT 1494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vuery Match 27.8%; Score 382.5; DB 8; Length 171; Best Local Similarity 35.8%; Pred. No. 9.2e-22; RESULT 1495
                                                                                PD 26-AUG-1986.

PA (KIRI ) KIRIN BREWERY KK.

Querry Match 27.9%; Score 384; DB 1; Length 269;

B88t Local Similarity 38.4%; Pred. No. 1.1e-21;

RESULT 1491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vuery Match 27.8%; Score 382; DB 2; Length 250; Best Local Similarity 38.4%; Pred. No. 1.5e-21; RESULT 1498
                                                                                                                                                                                                                                                                                                                  27.9%; Score 383; DB 2; Length 258; 34.3%; Pred. No. 1.3e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27.9%; Score 383; DB 2; Length 272; 33.9%; Pred. No. 1.4e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-MAR-2004.

1 (INCY-) INCYTE CORP.

Query Match

Best Local Similarity 35.5%; Pred. No. 1.2e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABM82642 standard; protein; 212 AA.
Human diagnostic and therapeutic pprotein SEQ ID NO:2891.
WO2004023973-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR05772 standard; protein; 250 AA.

Human adipsin gene product from the clone phg31.

W9006385-A.

14-JUN-1990.

(BETH-) BETH ISRAEL HOSPITAL ASSOC.

(DANA-) DANA-FARBER CANCER INST.

(META-) METABOLIC BIOSYSTEMS INC.

(BETH-) BETH ISRAEL HOSPITAL ASSOC.

Query Match

27.8%; Score 382; DB 2; Ler
Best Local Similarity 37.2%; Pred. No. 1.5e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 1493
ID AAU79393 standard; protein; 171 AA.
DE Novel human kallikrein KLK15, splice variant #3.
PN W0200214485-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADN10933 standard; protein; 171 AA.
Human kallikrein 15, marker of endocrine cancer.
WO20049285-A2.
(8-APR-2004.
(MOUN ) MOUNT SINAI HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADE58221 standard; protein; 263 AA.
Rat Protein AAB31922, SEQ ID NO 4092.
WO2003016475-A2.
                                                                                                                                                                                                                                                                                                                                                                  Snake venom ancrod polypeptide.
RESULT 1490

ID AAP61724 standard; protein; 269 AA.

DE Porcine elastase II.

POF1192289-A.

PD 26-AUG-1986.

PA (KIRI) KIRIN BREWERY KK.
                                                                                                                                                                                     AAR07513 standard; protein; 258 AA.
Ancrod-like polypeptide #2.
EP395375-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR05421 standard; protein; 250 AA.
Human adipsin/D encoded by a cDNA.
WO9001540-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-FEB-1990.
(CALB-) CALIF BIOTECHN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
RESULT 1497
                                                                                                                                                                                                                                                                                                                               Best Local Similarity RESULT 1492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                31-OCT-1990.
(GLAX ) GLAXO INC.
(KNOL ) KNOLL AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                        14-JUN-1990.
(BADI ) BASF AG.
(BACH/) BACH A.
                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PERE
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PD 27-FEB-2003.

PA (GEMO ) GEN HOSPITAL CORP.

PA (FARE ) BAYER AG.

Query Match

Best Local Similarity 37.6%; Pred. No. 1.9e-21;

RESULT 1499

ID ADN99596 standard; protein; 187 AA.

DE Novel human protein sequence #412.

PN WO2004038003-A2.

PD 06-MAY-2004.

PA (FIVE-) FIVE PRIME THERAPEUTICS INC.

QUERY Match

Best Local Similarity 42.7%; Pred. No. 1.7e-21;

RESULT 1500

ID ABN92049 standard; protein; 220 AA.

DE Human protein modification and maintenance molecule-29 (PMMM-29)

PN WO20031939-A2.

PD 17-APR-2003.

PD 17-APR-2003.

PD 17-APR-2003.

PD 17-APR-2003.

PD 27.6%; Score 379; DB 6; Length 187;

PA (FIVE-) FIVE GENOMICS INC.

QUERY MATCH

Best Local Similarity 37.2%; Pred. No. 2.2e-21;
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rattus norv
rattus norv
rattus norv
pangasius h
rattus norv
salmo salar
cavia porce
brachydanio
emaguinus oe
mus musculu
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brachydanio
dissostichu
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oreochromis
bos taurus
oreochromis
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sus scrofa
mus musculu
                                           homo sapien
struthio ca
xenopus lae
xenopus lae
homo sapien
                                                                                       homo sapien
mus musculu
mus musculu
mus musculu
bos taurus
m mus musculu
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2 Q6ZMR5 2 Q6IT10 Q64IT10 pseudonaj 2 Q6X143 Q64IT10 pseudonaj 2 Q18436 Q64IT10 Q64443 drosophil 2 Q18436 Q7Z163 Q7Z163 dermatoph Q7Z163 Q7PV05 Q7PV05 Q7PV05 Q7PV05 Q7PV05 A0Phales 2 Q7PVQ5 Q7PV07 A0Phales 2 Q7PVQ5 Q7PV07 A0Phales 2 Q7PVQ5 Q7PV07 A0Phales 2 Q7PVQ5 Q7PV07 A0Phales 2 Q7PVQ5 Q7PV07 A0Phales 2 Q7PVQ5 Q7PV07 A0Phales 2 Q7PVQ7 A0Phales	070092 070092 0700X6 0700X6 070002 070002 090019 090019	Q8MR00 Q7PZ88 Q7PZ88 Q7PZ88	Qebbii Q9VEA0 Q9vea0 Q9vea0 Q64ID4 Q64id4	Q9XY59 Q9VXC9 Q9VXC9	Q6W741 SER3 DROME P17207 O67550	070208 076954 076954 076954	Q8MJD1 Q8mjd1 Q8mjd1 Q6bd09	Q7PRK6 Q7PrK6 Q7PrK6 018450 018450 018450 018450	Q7Q6T0 Q27081 Q6X655 Q6X655	Q8MLC2 Q8mlc2 Q9vgb8 Q9vgb8 Q18443	070C37 079C37 070C59 079C529 081NG0 081nG0	Q7Q5K4 Q8MQS8 Q8mqs8	Q6XHU4 Q7PXJ1 Q9VT24 Q9VT24 Q9VE24	Q8MRL2 Q8mrl2 Q8mrl2 Q76920 Q76920	Q9NB77 Q9nb77 Q9nb77 Q9v886 Q9v886	Q8MUG0 Q8mug0 018442 018442	018447 018447 018447 018447 0702200 0702200 0702200	Q7PW15 Q7pw15 Q7pw15 Q9vrs7	O18655 O18655 Q8MS77 Q8ms77	Q6LU71 Q6lu71 Q6lu71 Q88Y93	Q9NGYS Q9ngyS	2,0054 QQ66V2 QQ66V2	Q/FWES Q1711 Q91711 Q91711 OBMCY4	001654 001654 001654	Q6GKZ6 Q6GKZ6 Q8IT49 Q8It49	094250 09VZS9 09VZB9 070L41 079L41	070NM2 Q/qnm2 an 070169 070169 mu
06ZMR5 06ZMR5 061110 061110 061110 061110 061113 018436 018436 072163 072163 072163 072163 072163 072163 072163 072163 072163 072163	2 Q7Q092 Q7Q092 2 Q7QKX6 Q74KK 2 Q7PV62 Q7PV62 2 Q9Y819 Q9Y819	2 Q8MR00 Q8mr00 2 Q7PZ88 Q7pz88	2 Q9VEA0 Q64ID4 Q64ID4	2 Q9VXC9 Q9vxc9	2 Q6W741 1 SER3 DROME P17207 2 O67550	2 Q70208 Q70208 2 076954 076954	2 Q8MJD1 Q8mjd1 2 Q6BD09 Q6bd09	2 Q7PRK6 Q7prk6 2 Q18450 018450	2 Q7Q6T0 2 Q27081 2 Q6X655 Q6x655	2 Q8MLC2 2 Q9VGB8 Q9vgb8 2 Q18443	2 070C37 07qC37 2 07Q529 07q529 2 081NG0	2 Q7Q5K4 Q7q5k4 2 Q8MQS8 Q8mqs8	2 QPRVJ1 Q6XNU4 2 Q7PXJ1 Q7PYJ1 2 Q9VT24 Q9vt24	2 Q8MRL2 Q8mrl2 2 Q76920 Q76920	2 Q9NB77 Q9nb77 Q9nb77 2 Q9v886	2 Q8MUG0 Q8mug0 2 O18442 O18442	2 Q18447 O18447 2 Q7Q2P0 Q7q2p0	2 Q7PW15 Q7pW15 2 Q9VRS7 Q9vrs7	2 O18655 O18655 2 Q8MS77 Q8ms77	2 Q6LU71 Q6lu71 2 Q8SY93 Q8SY93	2 Q9NGYS Q9ngyS	2 Q/qes4 2 Q966V2 2 Q9666V2	2 Q/FWE5 Q/FWE5 2 Q91711 Q91711 Q91711 Q91711	2 Quingra 2 001654 001654	2 Q6GKZ6 Q6GKZ6 2 Q81T49 Q81t49	2 Q9VZS9 Q9vZB9 2 Q9VZS9 Q9vZB9 2 Q7QL41 Q7q141	2 O/QNM2 O/QTM2 an 2 O/Q169 O/Q169 mu
8.6 421 2 Q6ZMR5 Q6ZML5 8.6 220 2 Q6XT10 Q6X110 Q6X1410 Q6X1430 Q6X1410 Q6X1410 Q6X1410 Q6X1410 Q6X1410 Q6X1410 Q6X1410 Q6X1431 Q7X163	8.5 357 2 Q7Q092 Q7Q092 8.5 357 2 Q7QKK6 Q74kK6 8.5 493 2 Q7PV62 Q7PV62 8.5 523 2 Q9V819 Q9V819	8.5 524 2 Q8MR00 Q8mr00 8.5 827 2 Q7P288 Q7P288 Q7P288	8.5 3.4 2 QOBADII QODUII 8.5 282 2 QOVEAO QOVOO 8.4 282 2 QG4ID4 Q64id4	8.4 242 2 Q9XY59 Q9Xy59 8.4 251 2 Q9VXC9 Q9vxc9	8.4 253 2 Q6W741 Q6W741 8.4 272 1 SER3 DROME P17207 8.4 287 2 067550 067550	8.4 245 2 070208 070208 8.4 245 2 076954 076954	8.4 282 2 Q8MJD1 Q8mjd1 8.4 324 2 Q6BD09 Q6bd09	8.3 235 2 Q7PRK6 Q7prk6 8.3 295 2 O18450 O18450	8.3 400 2 QYQSTO QYQSTO 8.3 400 2 Q270811 Q27081 8.3 186 2 Q8X655 Q6X651	8.3 266 2 QBMLC2 QBmlc2 8.3 267 2 Q9VGBB Q9vgbB 8.3 275 2 D18443 D18443	8.3 318 2 Q7QC37 Q7QC37 8.3 418 2 Q7QC39 Q7QC37 8.3 520 2 Q81VG0 Q81VG0	8.3 285 2 Q7Q5K4 Q7q5K4 8.3 405 2 Q8MQS8 Q8mqs8	8.2 2.6 2 Q6XH04 Q6XD04 8.2 2.6 2 Q7PYJ1 Q7PYJ1 8.2 2.68 2 Q9VT24 Q9vt24	8.2 305 2 Q8MRL2 Q8mr12 8.2 323 2 0.76920 0.76920	8.2 258 2 Q9VS86 Q9vs886	8.2 274 2 Q8MUG0 Q8mug0 8.2 253 2 Q18442 Q18442	8.2 258 2 Q7Q2P0 Q7Q2D0 Q7Q2D0	8.2 269 2 Q7PW15 Q7pw15 8.2 274 2 Q9VRS7 Q9vrs7	8.2 282 2 018655 018655 8.2 327 2 Q8MS77 Q8ms77	8.2 362 2 Q6LU71 Q6lu71 8.2 520 2 Q8SY93 Q8sy93	8.1 253 2 Q9NGYS Q9ngyS	8.1 340 2 Q/qos4 8.1 348 2 QQGGV2 QQGGV2	8.1 /14 / Q/FWES Q/DWES 8.1 296 / Q91711 Q91711 8.1 341 / OSMOYA	8.1 746 2 001654 001654 001654	8.0 141 2 Q6GKZ6 Q6gkz6 8.0 257 2 Q81T49 Q81t49	8.0 258 2 Q9VZE99 Q9VZE99 8.0 277 2 Q7Q141	8.0 277 2 Q7QNM2 Q7qnm2 an 8.0 367 2 O70169 O70169 mu
256 18.6 421 2 Q6ZMR5 Q6ZML5 256 18.6 422 2 Q6TT10 Q6T110 5.5 18.6 220 2 Q6TT10 Q6X143 5.5 18.6 254 2 Q18436 5.5 18.6 273 2 Q7ZL63 Q7ZL63 255 18.6 431 2 Q7PVQ5 Q7ZL63 255 18.6 292 2 Q7PVQ5 Q7PVQ5 255 18.6 405 2 Q7PVQ3 Q7PVQ5 256 18.6 292 2 Q7PVQ3 Q7PVQ4 257 18.5 254 2 Q1893	.5 18.5 357 2 Q7Q092 Q7Q092 .5 18.5 357 2 Q7QKK6 Q7QKK6 .5 18.5 493 2 Q7PV62 Q7PV62 .5 18.5 523 2 Q9V819 Q9V819	4.5 18.5 524 2 Q8NR00 Q8mr00 4.5 18.5 827 2 Q7PZ88 Q7PZ88 Q7PZ88	54 18.5 3.4 2 QUEDII QUEDII 55 18.5 33.4 2 QUVEAO QUEAO 55 18.4 282 2 QG41D4 QG41d4	253 18.4 242 2 Q9XY59 Q9xy59 253 18.4 251 2 Q9YXC9 Q9yxc9	53 18.4 253 2 Q6W741 Q6W741 53 18.4 277 1 SER3_DROME P17207 53 18.4 287 2 Q67550 067550	2.5 18.4 245.2 070208 070208 2.5 18.4 25.4 2 076954	.5 18.4 282 2 Q8MJD1 Q8mJd1 .5 18.4 324 2 Q6BD09 Q6bd09	52 18.3 235 2 Q7PRK6 Q7prk6 52 18.3 295 2 Q18450 Q18450 Q18450	252 18.3 401 2 Q70810 Q70810 152 18.3 400 2 Q77081 Q277081 155 18.3 186 2 Q6X655 Q6x655	1.5 18.3 266 2 QBMLC2 QBmlc2 1.5 18.3 267 2 Q9VGBB Q9VgBB Q9VgBB Q9VgBB NGA3	.5 18.3 318 2 070C37 079C37 .5 18.3 418 2 070529 079529 .5 18.3 520 2 081NG0 081NG0	251 18.3 285 2 Q7Q5K4 Q7q5K4 251 18.3 405 2 Q8MQS8 Q8mqs8	.5 18.2 246 2 Q0XHU4 Q0XHU4 Q0XHU4 .5 18.2 240 2 Q7PYJ1 Q7PYJ1 Q7PYJ1 .5 18.2 268 2 Q9VT24 Q9VE24	0.5 18.2 305 2 QBMRL2 QBmrl2 QBmrl2 O5 18.2 33.3 2 O76920 O76920 O76920	50 18.2 203 2 Q9NS96 091825 599886 50 18.2 258 2 Q9VS86 099886	250 18.2 274 2 Q8MUG0 Q8mug0 9.5 18.2 253 2 Q18442 Q18442	9.5 18.2 254 2 018447 9.5 18.2 258 2 Q7Q2P0 Q7q2p0	9.5 18.2 269 2 Q7PW15 Q7pw15 9.5 18.2 274 2 Q9VRS7 Q9vxs7	.5 18.2 282 2 018655 018655 .5 18.2 327 2 Q8MS77 Q8ms77	9.5 18.2 362 2 Q6LU71 Q6lu71 9.5 18.2 520 2 Q8SY93 Q8sy93	249 18.1 253 2 Q9NGYS Q9ngYS	49 10.1 303 2 Q4084 Q4084 49 18.1 388 2 Q966V2 Q966V2	99 18.1 /14 2 Q/FWE5 Q/FWE5 Q/FWE5 9.18.1 2.96 2 Q91711 Q91711 C91711 8.5 18.1 746 2 001654 001654 001654	48 18.0 141 2 Q6GKZ6 Q6gKz6 48 18.0 257 2 Q8IT49 Q81t49	48 18.0 257 2 070L41 0719141	48 18.0 <i>277</i> 2 Q7QNM2 Q7qnm2 an 48 18.0 367 2 O70169 O70169 mu	

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Escobar J., Flowers D., Fotopulos D., Garcia C., Georgescu A.M., A Glavina T., Gomez M., Gonzales E., Groza M., Hammon N., Hawkins T., Haydu L., Ho. H., Holler S., Groza M., Hammon N., Hawkins T., Haydu L., Holler S., Kahner K., Kimball H., Kobayashi A., Larionov V., Leem S.-H., Lopez F., Lou Y., Lowry S., Malfatti S., Martinez D., McCready P.M., Medina C., Morgan J., Nelson K., Nolam M., Ovcharenko I., Fitluck S., Pollard M., Popkie A.P., Predki P., Ouan G., Ramirez L., Rash S., Retterer J., Popkie A.P., Predki P., Quan G., Ramirez L., Rash S., Retterer J., Slezak T., Solovyev V., Thayer N., Tie Ramirez L., Rash S., Smith D., Slezak T., Solovyev V., Thayer N., Tie G., Yang J., Dubchak I., Serney T.S., DeJong P., Dickson M., Gordon D., Eichler E.E., Pennacchio L.A., Richardson P., Stubbs L., Rokhear D.S., Myers R.M., Rubin E.M., Lucas S.M.;

"The DNA sequence and biology of human chromosome 19.";

"The DNA sequence and biology of human chromosome 19.";

"The Jurekhariue Products: Secreted (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kallikrein 12.
Charge relay system (By similarity).
Charge relay system (By similarity).
Charge relay system (By similarity).
By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
N-linked (GlcNAc. ..) (Potential).
N-linked (GlcNAc. ..) (Potential).
KYUMIRMIMENN -> NSTLVGLGTSWNFNSCQPF (in
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PRINTS, PR00722; CHYMOTRYPSIN.
SWART; SM00020; Tryp SPC; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN HIS; 1.
Alternative splicing; Glycoprotein; Hydrolase; Serine protease;
                                                                                                                                                                                                                                                                                                        IsoId=Q9UKR0-2; Sequence=VSP_005403;
SIMILARITY: Belongs to the peptidase S1 family. Kallikrein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                             IsoId=Q9UKR0-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   isoform 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, AF135025, AR06065.1,
EMBL, AF343527, AAG3335.1,
EMBL, AX35824, AAQ8888.1,
HSSP, P00760, 1EZX.
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Genew; HGNC:6360; KLK12.
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62
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DISULFID
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SIGNAL
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BB473E98F8BAF703 CRC64;

005403

FTIG=VSP

248 AA; 26733 MW;

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STRANTE-SYBL/GAJ TISSUE=TONGUE;
The FANTOM CONSORTIUM.
The RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Tongue;
STRAIN=20499314; PubMed=11042159; DOI=10.1101/gr.145100;
MEDLINE=20499314; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                         1 MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTA
                                                                                                                                                                 61 AHCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLRLPVRV
                                                                        1 MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTA
                                                                                                                                                                                                                                      181 TSNMVCAGGVPGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDW
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STRAIN=CSTBL/66; TISSUE=Tongue;
STRAIN=CSTDL/66; TISSUE=Tongue;
MEDIINE; P., Hayashizaki Y.;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
                                                                                                                                                                                                                 121 TSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRI
                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus adult male tongue cDNA, RIKEN full-length enriched
11brary, clone:231008B01 product:similar to KALLIKKEIN 12 (EC
3.4.21.-) (KALLIKREIN-LIKE PROTEIN 5) (KLK-L5) (Fragment).
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0
 Length 248;
                                     Indels
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STRAIN=CS7BL/6J; TISSUE=Tongue;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
; Score 1374; DB 1;
; Pred. No. 3.5e-102;
0; Mismatches 0;
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 100.0%;
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 Query Match 100.
Best Local Similarity 100.
Matches 248; Conservative
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Carrained Strongers,

Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,

Arakawa T., Bono H., Carninci P., Pukuda S., Fukunishi Y., Furuno M.,

Arakawa T., Bono H., Carninci P., Pukuda S., Fukunishi Y., Furuno M.,

Anadaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,

A mada J., Kojima Y., Kono M., Izawa M., Kasukawa T., Kato H.,

A kawa J., Kojima Y., Kono H., Kouda M., Koya S., Kurihara C.,

A Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R.,

A sana H., Sasaki D., Shibata K., Shinata Y., Shinaki T.,

Sano H., Sasaki D., Shibata K., Shinata Y., Shinaki T.,

A sogabe Y., Suzuki H., Tagami M., Tagama A., Takahashi E., Tanaka T.,

A rejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,

A rejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,

A manateu M., Hayashizaki Y.;

B while Ako09217; BAB26143.1;

-1- SIMILARITY: Belongs to peptidase family S1.

B while Ako09217; BAB26143.1;

-1- SIMILARIY: Belongs to peptidase family S1.

B while Ako09217; PROJ S.,

MCD: MC1.000 to the EMBL/GenBank/DDBJ databases.

C GO:0004285; Fchymotrypsin activity; IEA.

GO: GO:0004285; Fchymotrypsin activity; IEA.

GO: GO:0004285; Fchymotrypsin activity; IEA.

GO: GO:0006508; P:proteldase activity; IEA.

GO: GO:0006508; P:proteldase S1.

R InterPro: IPR00134; Peptidase S1.

R InterPro: IPR00134; Peptidase S1.

R InterPro: IPR001314; Peptidase S1.

R InterPro: IPR001314; Peptidase S1.

R Ffam: PP00089; Trvosin: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74 EHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPVRVTSSVQPLPLPNDC 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 EHSLTKLDWTEQLRHTTFSITHPSYQGAYQNHEHDLRLLRLNRPIHLTRAVRPVALPSSC 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  134 ATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRITSNMVCAGGVPGQ 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 VTTGAMCHVSGWGTTNKPWDPFPDRLQCLNLSTVSNETCRAVFPGRVTENMLCAGGEAGK 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 LSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAHCSGSRYWVRLG
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               MEDLINE-20530913; PubMed=11076861; DOI=10.1101/gr.152600; Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Aizawa K., Nagaoka J., Sasaki N., Carninci P., Sumi N., Ishi Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watshiwagi K., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Rike integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
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PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM0020; Tryp.SPS: 1.
PROSITE; PS50240; TRYPSIN.DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; UNKNOWN 1.
PROSITE; PS00135; TRYPSIN EER; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [6]
SEQUENCE FROM N.A.
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KLK8 HUMAN RESULT 3

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0602<u>5</u>9; Q9HCB3; Q9UIL9; Q9UQ47;
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Neuropsin precursor (EC 3.4.21..) (NP) (Kallikrein 8) (Ovasin) (Serine protease TADG-14) (Tumor-associated differentially expressed gene-14 protein) (UNQ283/PR0322).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O'Brien T.J.;
"Cloning of tumor-associated differentially expressed gene-14, a novel
serine protease overexpressed by ovarian carcinoma.";
Cancer Res. 59:4435-4439(1999).
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Lamerdin J.B., McCready P.M., Skowronski B., Viswanathan V.,
Burkhart-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S.,
Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Garnes J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Brain;
MEDLINE=99203457; PubMed=10102990;
Mitsui S., Tsurnoka N., Yamashiro K., Nakazato H., Yamaguchi N.;
Mitsui S., Tsurnoka N., Yamashiro K., Nakazato H., Yamaguchi N.;
A novel form of human neuropsin, a brain-related serine protease, is generated by alternative splicing and is expressed preferentially in human adult brain.";
                                                                                                                                                                                                                                                                                                                                       TISSUE-Hippocampus;
MEDLINE-98132070; PubMed=9714609; DOI=10.1016/S0378-1119(98)00232-7;
Yobhida S., Taniguchi M., Hirata A., Shiosaka S.;
"Sequence analysis and expression of human neuropsin cDNA and gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003; MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003; Clark H.F., Gurney A.L., Abaya B., Baker K., Baldwin D., Brush J., Chow B., Chui C., Crowley C., Currell B., Douel B., Dowd P., Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.B., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Liao D., Mark M., Robbie B., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D., Vi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I., Godowski P., Gray A., The secreted pictorial discovery initiative (SPDI), a large-scale for the secreted pictorial discovery initiative (SPDI), a large-scale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 effort to identify novel human secreted and transmembrane proteins:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gan L., Gelinas R., Gown A.M., Moss P., Smith R., Wang K.;
Moleccular cloning and characterization of a novel serine protease,
ovasin, a potential molecular marker for ovarian cardinomas.";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM 1).
PubMed=11054574; DOI=10.1016/S0378-1119(00)00382-6;
Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,
Moss P., Paeper B., Wang K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Underwood L.J., Tanimoto H., Wang Y., Shigemasa K., Parmley T.H.,
                                                                                                                                                                                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Moss P., Paeper B., Wang K.; "Sequencing and expression analysis of the serine protease gene cluster located in chromosome 19q13 region.";
                                                                                                                                                                 procein, tungzes/rwosza;.
Name=KLK8; Synonyms=NRPN, PRSS19, TADG14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99413504; PubMed=10485494;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eur. J. Biochem. 260:627-634(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM 1).
TISSUE=Ovary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM 1).
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                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene 257:119-130(2000).
                                                                                                                                                                                                     (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene 213:9-16(1998).
                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                       Homo sapiens
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By similarity.
By similarity.
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By similarity.
By similarity.
A -> AACGSLDLIKLYAENLPCWHINPOWPSQPSHCPRG
Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S., Andreise T., Trankheim M., Attix C., Amico-Keller G., Coefield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B., Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A., Olsen A.S., Carrano A.V.;
"Sequence analysis of chromosome 19q13.4.";
"Sequence analysis of chromosome 19q13.4.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
-!-FUNCTION: Suggested to be involved in kindling epileptogenesis and hippocampal plasticity.
-!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-, Lys-.
-!- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                           expressed in the
                                                                                                                                                                                                                                                                     Isoid=060259-2; Sequence=VSP 005401;
TISSUE SPECIFICITY: Isoform 1 is predominantly expressed in TISSUE SPECIFICITY: Isoform 1 is expressed in adult brain and hippocampus. Both forms are also found in fetal brain and placenta. Not detected in kidney, spleen, liver and lung. SIMILARITY: Belongs to the peptidase SI family. Kallikrein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alternative splicing, Glycoprotein, Hydrolase, Serine protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MIM; 605644; -. GO: 6008236; F: serine-type peptidase activity; TAS. GO: 0007399; P: neurogenesis; TAS.
                                                                                                                                                                                                         Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        similarity.
                                                                                                                                                                                                                                        IsoId=O60259-1; Sequence=Displayed;
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Neuropsin.
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InterPro; IPR001254; Peptidase S1.
InterPro; IPR001314; Peptidase_S1A.
Pfam; PP00089; Trypsin; 1.
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PROSITE: PS50240; TRYPSIN DOM; 1.
PROSITE: PS00134; TRYPSIN H15; 1.
PROSITE: PS00135; TRYPSIN SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, AB009849; BAA28673.1;
EMBL, AB012761; BAA28676.1;
EMBL, AB010780; BAA88684.1;
EMBL, AB008927; BAA82665.1;
EMBL, AB008927; BAA82666.1;
EMBL, AF055982; AAD56050.1;
EMBL, AF095742; AAD55979.1;
EMBL, AF243527; AAD29574.1;
EMBL, AX359035; AAQ83351.1;
EMBL; AX359035; AAQ83351.1;
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RAY MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wann J., Hsieh F.,
RA Brownstein M.J., Usdin T.B., Tochiyuki S., Carninci P., Frange C.,
RA Brownstein M.J., Usdin T.B., Tochiyuki S., Carninci P., Prange C.,
RA Basak S.A., McKenan R.J., Malam R.J., Malahy S.J.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millahy S.J.,
Rosak S.A., McWann P.J., McKernan K.J., Malek J.A., Gunzarene P.H.,
RA Richards S., Worley K.C., Hale S., Garchen R.J., Lu X., Gibbs R.A.,
Rahay J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Mhiting M. Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Ray Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Dones S.J., Marra M.A.,
R. Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                          192
                                                                                                                                                                                                                                                            62 HCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGAST-SHEHDLRLLRLRLPVRV 120
                                                                                                                                                                                                                                                                                    3 HCKKPKYTVRLGDHSLQNKDGPEQEIPVVQSIPHPCYNSSDVEDHNHDLMLLQLRDQASL 132
                                                                                                                                                                                                                                                                                                                                               180
                                                                                                                                                                                                                                                                                                                                                                                                                                    181 TSNMVCAGGVPGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDM 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               251
                                                                                                                                                                           61
                                                                                                                                                                                                                 13 MFLLLLGGAWAGHSRAQEDKVLGGHECQPHSQPWQAALFQGQQLLCGGVLVGGNWVLTAA 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                           193 TDGMVCAGSSKGADTCQGDSGGPLVCDGALQGITSWGS-DPCGRSDKPGVYTNICRYLDW
                                                                                                                                                                                                                                                                                                                                               121 TSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRI
                                                                                                                                                                        5 IFLLL --- CVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAA
                                                                                                                                                                                                                                                                                                                                                                                     133 GSKVKPISLADHCTQPGQKCTVSGWGTVTSPRENFPDTLNCAEVKIFPQKKCEDAYPGQI
                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                2,
                                                                                     260;
                                                                                     DB 1; Length
                                                                                                                                Indels
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                  /FTId=VSP 005401.
28048 MW; EF439E5B8C83E660 CRC64;
WRSNPLPPAA (in isoform 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) Kallikrein 8, isoform 1 preproprotein.
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                                                                                   Query Match 45.9%; Score 630.5; DB 1;
Best Local Similarity 50.2%; Pred. No. 1.3e-42;
Matches 123; Conservative 24; Mismatches 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          260 AA.
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                                          260 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=KLK8;
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133 GSKVKPISLADHCTQPGQKCTVSGWGTVTSPRENFPDTLNCAEVKIFPQKKCEDAYPGQI 192
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                                                                                                                                                                                                                                                                                                                                                                                                           193 TDVMVCAGSSKGADTCQGDSGGPLVCDGALQGITSWGS-DPCGRSDKPGVYTNICRYLDW 251
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                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=BALB/C; TISSUE-Hippocampus; MEDLINE=95348817; PubMed=7623137; Chen Z.-L. Yoshida S., Kato K., Momota Y., Suzuki J., Tanaka T., Tto J., Nishino H., Aimoto S., Kiyama H., Shiosaka S.; "Expression and activity-dependent changes of a novel limbic-serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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S
                                                                                                                                                                                                   45.7%; Score 627.5; DB 2; Length 260; 50.2%; Pred. No. 2.2e-42;
                                                                                                                                                                                                                            93; Indels
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       GO, GO.0004263; F:chymotrypsin activity; IEA.
GO, GO.0004285; F:chymotrypsin activity; IEA.
GO, GO.0004295; F:trypain activity; IEA.
GO, GO.0004295; F:trypain activity; IEA.
GO, GO.0006289; P:trypain activity; IEA.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR00903; Pept_Ser_Cys.
Pfam; PP00089; Trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SWART; SM00020; Tryp_SFC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
                                                                                                                                                                 Hydrolase; Protease; Serine protease.
SEQUENCE 260 AA; 28090 MW; EF5934EB96295660 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Neuropsin precursor (EC 3.4.21.-) (NP) (Kallikrein 8)
Name=Klk8, Synonyms=Nrpn, Prss19;
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              260 AA
                                                                                                                                                                                                                            Matches 123; Conservative 24; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protease gene in the hippocampus.";
J. Neurosci. 15:5088-5097(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                 Best Local Similarity
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SEQUENCE FROM N.A.
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Q61955;
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Strausperg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jordan H., Moore T., Max S. I., Wang J., Haidh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Romnstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Rana S.S., McZhan P.J., McKernan R.J., Malek J.A., Gunarane P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield X.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
C. M. M. M. A., Schein J.E., Jones S.J.M., Marra M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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J. Biol. Chem. 274:4220-4224(1999).
-!- FUNCTION: Suggested to be involved in kindling epileptogenesis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- TISSUE SPECIFICITY: Expressed specifically in the limbic system of mouse brain and is localized at highest concentration in pyramidal neurons of the hippocampal CA1-3 subfields.
-!- MASS SPECIFOMETRY: WW-26613; METHOD=MALDI; RANGE=29-260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-, Lys-.
-!- ENZYME REGULATION: Strongly inhibited by diisopropyl
fluorophosphate, leupeptin and (4-amidinophenyl)methanesulfonyl 1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hippocampal plasticity. Has a strong proteolytic activity against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shimizu C., Yoshida S., Shibata M., Kato K., Momota Y., Matsumoto K., Shiosaka T., Midorikawa R., Kamachi T., Kawabe A., Shiosaka S.; "Characterization of recombinant and brain neuropsin, a plasticity-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Hippocampus;
MEDLINE-9913451; PubMed=9933620; DOI=10.1074/jbc.274.7.4220;
Kishi T., Kato M., Shimizu T., Kato K., Matsumoto K., Yoshida S.,
Shiosaka S., Hakoshima T.;
"Crystal structure of neuropsin, a hippocampal protease involved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF N-TERMINUS, CHARACTERIZATION, AND MASS SPECTROMETRY.
STRAIN=BALB/c; TISSUE=Brain;
MEDLINE=98225202; PubMed=9556608; DOI=10.1074/jbc.273.18.11189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: Belongs to the peptidase S1 family. Kallikrein
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnag.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- MASS SPECTROMETRY: MW=26229; METHOD=MALDI; RANGE=33-260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 33-257.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lated serine protease.";
Biol. Chem. 273:11189-11196(1998).
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PDB; INPM; X-ray; A/B=33-256.
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EMBL; BC055895; AAH55895.1;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                     240
TSNMVCAGGVPGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDW
                                    121 TSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRI
                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. NCEL_TaxID=10116;
                                                                                                                                                                                                                                                15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Neuropsin precursor (BC 3.4.21.-) (NP) (Kallikrein 8) (Brain serine protease 1).
Name-Klk8; Synonyms-Bspl, Nrpn, Prss19;
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Neuropsin.
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PRINTS; PRO0722; CHYMOTRYPSIN.
SMART; SMO0202; CHYMOTRYPSIN.
PROSTTE; PS00136; TRYPSIN_DOM; 1.
PROSTTE; PS00134; TRYPSIN_BER; 1.
PROSTTE; PS00135; TRYPSIN_BER; 1.
PROSTTE; PS00135; TRYPSIN_BER; 1.
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Interpro, IPR001254; Peptidase S1.
Interpro, IPR001314; Peptidase SIA.
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STRAIN=Fischer; TISSUE=Brain;
                                                                                                                                                                                                                           STANDARD;
                                                                                                                                      241 IRMIMRN 247
                                                                                                                                                               252 IKKTMDN 258
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InterPro; IPR001254; Peptidase_S1.
Pfan; PF00089; TYD1314; Peptidase_S1A.
Pfan; PF00089; TYD1314; Peptidase_S1A.
PRO0722; CHYMOTRYPSIN.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00135; TRYPSIN SRR; 1.
PROSITE; PS00135; TRYPSIN SRR; 1.
                                                                                                                                                  similarity).
similarity).
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SIGNAL 1 28
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-!- SUBCELLULAR LOCATION: Secreted
    123 SVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRITS 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          183 NMVCAGGVPGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDWIR 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              195 GMVCAGSSNGADICQGDSGGPLVCNGVLQGITTWGS-DPCGKPEKPGVYTKICRYTNWIK 253
                                                                                                                                                                                                                                                                                                                                                                              64 SGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGAS-TSHEHDLRLLRLRLPVRVTS 122
                                                                                                                                                                                                                                                                                                                                                                                                                       75 KKDKYSVRLGDHSLQKRDEPEQEIQVARSIQHPCFNSSNPEDHSHDIMLIRLQNSANLGD 134
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LFLLMGAWAGLTRAQGSKILEGOECKPHSQPWQTALFQGERLVCGGVLVGDRWVLTAAHC
                                                                                                                                                                                                                                                                                         5 IFLLL-CVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAHC
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MEDLINE=20329229; PubMed=10872828; DOI=10.1006/bbrc.2000.2761;
Mitsui S., Yamada T., Okui A., Kominami K., Uemura H., Yamaguchi N.;
"A novel isoform of a kallikrein-like protease, TLSP/hippostasin,
(PRSS20), is expressed in the human brain and prostate.";
Biochem. Biophys. Res. Commun. 272:205-211(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Hippocampus;
MEDLINE-96438138; PubMed=9765601; DOI=10.1016/S0167-4781(98)00116-X;
YOSHIGH S., Taniguchi M., Suemoto T., Oka T., He X.P., Shiosaka S.;
"CDNA cloning and expression of a novel serine protease, TLSP.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9UBX7; 075837; 09N865; 16-0CT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 25-0CT-2004 (Rel. 45, Last annotation update) Kallikrein 11 precursor (EC 3.4.21.-) (Hippostasin) (Trypsin-like protease) (UNQ649/PRO1279). Name=KLAII; synonyms=PRSS20, TLSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
173 By similarity.
74 By similarity.
246 By similarity.
218 By similarity.
198 By similarity.
233 By similarity.
245 By similarity.
25510 MW, 58DF4F0602A0B7F5 CRC64;
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MEDLINE=20130117; PubMed=10662548; DOI=10.1006/geno.1999.6072;
Yousef G.M., Scorilas A., Diamandis E.P.;
                                                                                                                                                                                                  Score 621.5; DB 1; Length 260; Pred. No. 6.7e-42;
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                                                                                                                                                         260 AA;
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                           DISULPID
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

X. TISSUB=Testis;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

X. Straubberg R.L.; Feingold B.A.; Grouse L.H.; Derge J.G.;

X. Altsubner R.D.; Collins F.S.; Wagner L., Shenmen C.M.; Bata N.K.;

X. Altschul S.F.; Zeeberg B., Buetow K.H.; Schaefer C.F.; Bhat N.K.;

X. Altschul S.F.; Jordan H.; Moore T., Max S.I.; Wang J.; Haiteh F.;

X. Hopkins R.F.; Jordan H.; Moore T., Max S.I.; Wang J.; Haiteh F.;

X. Aspleton M.; Soares M.B.; Bonaldo M.F.; Casavant T.L.; Scheetz T.E.;

X. Brownstein M.J.; Usdin T.B.; Toshiyuki S.; Carninci P.; Prange C.;

X. Bosak S.A.; Morley K.C.; Hale S.; Garcia A.M.; Gay L.J.; Hulyk S.W.;

X. Milalon D.K.; Muzny D.M.; Sodergren E.J.; Lu X.; Gibbs R.A.;

X. Whiting M.; Madan A.; Young A.C.; Shevchenko Y.; Bouffard G.G.;

X. Blakesley R.W.; Touchman J.W.; Green E.D.; Dickson M.C.;

X. Rodriguez A.C.; Garrimwood J.; Schmutz J.; Myers R.M.;

X. Butterfield Y.S. N.; Krzywinski M.I.; Skalska U.; Smailus D.E.;

X. Generation and initial analysis of more than 15,000 full-length human
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RA Grimwood J., Gordon L.A., Olsen A.S., Terry A., Schmutz J.,

RA Grimwood J., Gordon L.A., Olsen A.S., Terry A., Schmutz J.,

RA Lamerdin J.E., Hellsten U., Goodstein D., Couronne O., Tran-Gyamfi M.,

RA Aerts A., Altherr M., Ashworth L., Bajorek E., Black S., Branscomb E.,

RA Aerts A., Altherr M., Caoile C., Chan Y.M., Christensen M.,

RA Cleland C.A., Copeland A., Dalin E., Denal P., Denys M., Detter J.C.,

RA Escobar J., Flowers D., Fotopulos D., Garcia C., Georgeecu A.M.,

RA Glavina T., Gomez M., Gonzales E., Groza M., Hammon N., Hawkins T.,

RA Haydu L., Ho I., Huang W., Israni S., Jett J., Kadner K., Kimball H.,

RA Kobayashi A., Larionov V., Leem S.-H., Lopez F., Lou Y., Lowry S.,

RA Malfatti S., Martinez D., McCready P.M., Medina C., Morgan J.,

RA Nelson K., Nolan M., Ovcharenko I., Pitluck S., Pollard M.,

RA Popkie A.P., Predki P., Quan G., Ramirez L., Rash S., Retterer J.,

RA Rodriguez A., Rogers S., Salamov A., Salazar A., She X., Smith D.,

RA Slezak T., Solovyev V., Thayer N., Tice H., Tsai M., Ustaszewska A.,

RA Furey T.S., DeJong P., Dickson M., Gordon D., Eichler E.E.,

RA Furey T.S., Myers R.M.,

RA Furey C., Nochar D.S., Nyers R.M.,

RA Furey T.S., Myers R.M.,
                                                                                                                                                                                                                                                                                                                                           MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
A Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
Chen J., Chow B., Chui C., Crowley C., Currell B., Douel B., Dowd P.,
A Eaton D., Roster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
A Huang A., Kim H.S., Kilmowski L., Johnson S., Lee J.,
Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
Vi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
Godowski P., Gray A.;
"The secreted protein discovery initiative (SPDI), a large-scale
effort to identify novel human secreted and transmembrane proteins: a
first condentify novel human secreted and transmembrane proteins: a
Gonome Res. 13:2265-2270(2003).
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

-!- FUNCTION: Possible multifunctional protease. Efficiently cleaves
bz-Phe-Arg-4-methylconmaryl-7-amide, a kallikrein substrate, and
weakly cleaves other substrates for kallikrein and trypsin.
Rubin E.M., Lucas S.M.; "The DNA sequence and biology of human chromosome 19.";
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CKRPRYIVHLGQHNLQKEEGCEGTRTATESFPHPGFNNSLPNKDHRNDIMLVYMASPVSI 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 KIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAHCSGSRYWVRLGEHSLSQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 KLLEGEECAPHSÓPWÓVALYERGRFNCGASLISPHWYLSAAHCOSRFMRVRLGEHNLRKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21094033; PubMed=11177570; DOI=10.1089/104454900750058080; Olsson A.Y., Persson A.M., Valtonen-Andre C., Lundwall A.; "Glandular Kallikreins of the cotton-top tamarin: molecular cloning the gene encoding the tissue kallikrein."; DNA Cell Biol. 19:721-727(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saguinus oedipus (Cotton-top tamarin).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Platyrrhini, Callitrichidae, Saguinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases C -1- SIMILARITY: Belongs to peptidase family S1.

EMBL, ARI/Ja845; AAS45302.1; -.

RESP; P00761; 1AKS.

GO: GO:0004263; F:chymotrypsin activity; IEA.

GO: GO:0004295; F:crypsin activity; IEA.

GO: GO:0004295; F:crypsin activity; IEA.

RO: GO:0006508; P:proteolysis and peptidolysis; IEA.

R HIGEPRO: IPR001354; Peptidase S1.

InterPro: IPR001314; Peptidase S1.

R Pfam; PF00089; Trypsin; 1.

R Pfam; PF00089; Trypsin; 1.

R PROSITE; PS00240; TRYPSIN DOM; 1.

R PROSITE; PS50240; TRYPSIN DOM; 1.

R PROSITE; PS50240; TRYPSIN DOM; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44.5%; Score 611; DB 2;
49.4%; Pred. No. 4.6e-41;
iive 31; Mismatches 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                   255 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                        240 WIRMIMRNN 248
                                                                                                                                                                                                                                                                                                      242 WIQETMKNN 250
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es 118; Conserv
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                                                                          121
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                                                                                                                                                                                                                                                                                                                                                                                                                                         97JIG6
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                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                              Isoid=Q9UBX7-2; Sequence=VSP 005402;
TISSUE SPECIFICITY: Expressed in brain, skin and prostate. Isoform
1 is expressed preferentially in brain; isoform 2 in prostate.
SIMILARITY: Belongs to the peptidase SI family. Kallikrein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 LSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAH
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(By similarity).
(By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO, GO:0008236; F:serine-type peptidase activity; TAS.
InterPro; IPR009003; Pept_Ser_Cys.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001214; Peptidase_S1A.
Pfam; PF00089; Trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PROSITE; PS00134; TRYPSIN INS; 1.
PROSITE; PS00134; TRYPSIN INS; 1.
PROSITE; PS00135; TRYPSIN INS; 1.
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Kallikrein 11.
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                    Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 618.5; DB 1; Pred. No. 1.1e-41; 35; Mismatches 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (in isoform 2)
                                                                  IsoId=Q9UBX7-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, AB012917; BAA33404.1; ALT_INIT.
EMBL, AB01373; BAA88713.1; -
EMBL, AB041036; BAA96797.1; -
EMBL, AP16462; AA047815.1; -
EMBL, AP24357; AA033364.1; -
EMBL, AP359014, AA089333.1; -
EMBL, AC011473, AA023257.1; -
EMBL; BC022068; AA422068.1; -
EMBL; BC072058; AA12068.1; -
EMBL; BC072058; AA12068.1; -
EMBL; BC072058; AA12068.1; -
EMBL; BC072058; AA12068.1; -
EMBL; BC072058; ALXII.
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SIGNAL
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61 CQTRFWRVRLGEHNLRKFDGPEQLRSVSRIIPHPGY--EARTHRHDIMLLRLFKPARLTA 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 IFLLLCVLGLSQAAT -- PKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAH
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                               Olsson A.Y., Lundwall A.; "Organization and evolution of the glandular kallikrein locus in Mus musculus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 254;
                                                                                                                                                                                                                                                                                                                                                     MEROPS; SOL 207; ---
MEROPS; SOL 207; ---
MGD; MGT:244753; Klk15.
MGD; MGT:244753; Klk15.
MGD; MGCO004263; F:chymotrypain activity; IEA.
GG; GG:0004225; F:trypain activity; IEA.
GG; GG:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPRO0124; Peptidase_SlA.
InterPro; IPRO0134; Peptidase_SlA.
InterPro; IPRO0003; Pept_Ser_Gys.
Fean; PF00009; Trypsin; 1.
RPINTS; PR00722; CHYMOTRYPSIN.
SWART; SM00020; Tryp_SPC; 1.
RPOSITE; PS00134; TRYPSIN DOM; 1.
RPOSITE; PS00134; TRYPSIN DIS; UNKNOWN_1.
RPOSITE; PS00134; TRYPSIN HIS; UNKNOWN_1.
RPOSITE; PS00134; TRYPSIN HIS; UNKNOWN_1.
RPOSITE; PS00134; TRYPSIN SER:
RHOGINES: PS00134; TRYPSIN SER:
RHOGINES: SS00134; TRYPSIN SER:
RHOGINES: PS00134; TRYPSIN SER:
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RHOGINES: PS00135; TRYPSIN SER:
RHOGINES: PS00135; TRYPSIN SER:
RHOGINES: PS00135; TRYPSI
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Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                databases.
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                                                                                                                        Biochem. Biophys. Res. Commun. 299:305-311(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 44.3%; Score 608; DB 2; Local Similarity 49.0%; Pred. No. 7.9e-41; Les 124; Conservative 30; Mismatches 77.
                                                                                                                                                                                                                                                                      to peptidase family S1
                                                                                                                                                                          SEQUENCE FROM N.A.
Adams M., Mural R.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      275 AA
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01-MAR-2003 (TrEMBLrel. 23, Last seq
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01-MAR-2004 (TrEMBLrel. 26, Last
Variant form hippostasin/KLK11.
Name-KLK11;
                                                                                                                                                                                                                                             -!- SIMILARIY: Belongs to the EMEL, AY152434; BAN78422.1; HSSP; P00760. 'PPW
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Matches 124; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        235 GVYTKVCSYLEWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRITSN 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MVCAG-GVPGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDWIR 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGA--STSHEHDLRLLRLRLPVRVTSS 123
   248
                                  198 GRGAESCEGDSGGPLVCGGILQGIVSWGDV-PCDNTTKPGVYTKVCRYVKWIRETWKRN 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 FLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAHCSG 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 PIALALVTGHVGGETRIIKGYECRPHSQPWQVALFQKTRLLCGATLIAPKWLLTAAHCRK 65
                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
   191 -PGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDWIRMINN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
PubMed=15203212; DOI=10.1016/j.ygeno.2004.01.009;
Olsson A.Y., Lilja H., Lundwall A.;
"Taxon-specific evolution of glandular kallikrein genes and identification of a progenitor of prostate-specific antigen.";
Genomics 84:147-156(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- MISCELLANEOUS: The sequence shown here is derived from an EMBL/GenBank/DDBJ third party annotation (TPA) entry. EMBL; BK001364; DAA05600.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 44.4%; Score 610; DB 2; Length 250; Best Local Similarity 46.7%; Pred. No. 5.4e-41; Matches 115; Conservative 37; Mismatches 90; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  glandular kallikrein 11.
; 247B29D3F0DEF8F1 CRC64;
                                                                                                                                                                                                                                                                      25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                     Glandular kallikrein 11 precursor.
Name=Klk11;
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22 250 G<sup>2</sup>
250 AA; 27630 MW;
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                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat)
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SEQUENCE FROM N.A.
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QBCGR4;
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                                                                                                                                                                                                                Q632F2
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08CCR4
AC QBCGR
DT 01-MA
DT 01-MA
DT 01-MA
DE Prost
GN Name=
GN Eukar
OC Mamma
OC Mamma
OC Mamma
CO Mamma
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OC Mamma
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0632E2
AC 0632E
AC 0632E
DT 25-00
DT 25-00
DT 25-00
DE Glan GS Rattl
CS NABIL
RN RAT 11]
RN PUBM
RA OLBEM
RA OLBEM
RY GGNO
CC -1-1
DR EMBL
KW SIGN
FT SIGN
SEQUIN
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Homo sapiens (Human)
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TISSUB-PCR rescued clones;
MEDLINE-22388251; PubMed-12477932; DOI=10.1073/pnas.242603899;
Attausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.R., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Appkins R.F., Jordan H., Moore T., Mang J., Hsieh F.,
Appleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Stapleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Arapleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
And S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Astchards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 CLKPWVSLTSPTHVSPDLSSSNYCLSHLSRYIVHLGQHNLQKEEGCEQTRTATESFPHPG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98 YLGA--STSHEHDLRLLRLRLPVRVTSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPF 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PDLLQCLNLSIVSHATCHGVYPGRITSNMVCAG-GVPGQDACQGDSGGPLVCGGVLQGLV 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          183 PHTLRCANITIIEHQKCENAYPGNITDTMVCASVQEGGKDSCQGDSGGPLVCNQSLQGII 242
                                                                                                                                                                                                                                                                                                                                                                                              62
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                                                                                                                                                                                                                                                                                                                                                                                                               CSG------SRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPG
                                                                                                                                                                                                                                                                                                                                                                                            3 LSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAH
                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                             30;
                                                                                                                                                                                                                                                                                                                           43.7%; Score 601; DB 2; Length 275; 44.2%; Pred. No. 3.1e-40; ive 35; Mismatches 88; Indels
                                                                                                                                                                                                                                                                             Hydrolase; Protease; Serine protease.
SEQUENCE 275 AA; 30165 MW; 257A42B28F40E2C4 CRC64;
                                                        GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0004293; F:chymotrypsin activity; IEA.
GO; GO:00064295; F:trypsin activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR001354; Peptidase S1.
InterPro; IPR001314; Peptidase S1.
InterPro; IPR00903; Peptidase S1.
InterPro; IPR009003; Peptidase S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 28, Last annotation update)
Kallikrain 15, isoform 4 preproprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             215 SWGSVGPCGQDGIPGVYTYICKYVDWIRMIMRNN 248
               to peptidase family S1
                                                                                                                                                                        PERMIS PRO0009; TYPBIN; 1.
PRINTS, PRO0722; CHYMOTRYPSIN.
SMART; SMO0200; TYP, SPC; 1.
PROSITE; PSS0240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HS; UNKNOWN 1.
PROSITE; PS00135; TRYPSIN HS; 1.
-i- SIMILARITY: Belongs to F
EMBL; AB078780; BAC54105.1;
HSSP; P00760.107
                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 44.28
Matches 121; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                             Query Match
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061810
DC 061810
DT 05-JU
DT 05-JU
DT 25-OC
DE KAILLI
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64 SGSRYWVRLGEHSLSQLDWTEQIRHSGPSVTHPGYLGASTSHEHDLRLLRLRLPVRVTSS 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 KSYPGRLTNTWYCAGAEGRGAESCEGDSGGPLVCGGILQGIVSWGDV-PCDNTTKPGVYT 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62
                                                                                                                                    Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 LLLTLSFLLASTAQDGDKLLEGDECAPHSQPWQVALYERGRFNCGASLISPHWVLSAAHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 VQPLPLPNDCATAGTECHVSGWGITNH-----PRN--PFPDLLQCLNLSIVSHATCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 LLCVLGLSQAAT----PKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=11010966; DÓI=10.1074/jbc.M005432200;
Yousef G.M., Scorilas A., Jung K., Ashworth L.K., Diamandis E.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata, Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hase; FUVIAL ALANS.

GO; GO: 0004295; F: Crypsin activity; IEA.

GO; GO: 0004295; F: trypsin activity; IEA.

GO; GO: 0005608; P: proteolysis and peptidolysis; IEA.

InterPro; IPR001254; Peptidase S1A.

InterPro; IPR001314; Peptidase S1A.

InterPro; IPR009003; Peptidase S1A.

InterPro; IPR009003; Peptidase S1A.

InterPro; IPR009003; Peptidase S1A.

InterPro; IPR001314; Peptidase S1A.

PRNNTS; PR00722; CHYMOTRYPSIN.

SWART; SMO0722; TRYPSIN DOM; 1.

PROSITE; PS00134; TRYPSIN DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 255 AA; 28016 MW; 1581B784D4A39C4F CRC64;
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Q9H2R5; Q15358; Q9H2R4; Q9H2R6; Q9HBG9;
16-0CT-2010 (Rel. 40, Created)
16-0CT-2010 (Rel. 40, Last sequence update)
25-0CT-2004 (Rel. 45, Last annotation update)
Kallikrein 15 precursor (EC 3.4.21.-) (ACO protease).
                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43.6%; Score 599; DB 2;
46.9%; Pred. No. 4.2e-40;
tive 32; Mismatches 86
                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
TISSUE=PCR rescued clones;
Director MGC Project;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                             to peptidase family
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; BC069518; AAH69518:1; --
EMBL; BC069480; AAH69480:1; --
HSSP; P00761; 1AKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata;
Mammalia; Butheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       233 YICKYVDWIRMIMRNN 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240 KVCHYLEWIRETMKRN 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 46.9
Matches 120; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=Q9H2R5-4; Sequence=VSP_005404;
TISSUE SPECIFICITY: Highest expression in the thyroid gland. Also
expressed in the prostate, salivary, and adrenal glands and in the
colon testis and kidney.
SIMILARITY: Belongs to the peptidase S1 family. Kallikrein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=Q9H2R5-2; Sequence=VSP 005405;
Note=May be produced at very low levels due to a premature stop
codon in the mRNA, leading to nonsense-mediated mRNA decay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               not yet known
                                                                                                                                                                                                                                                                                                               MEDLINE=94289486; PubMed=8018728; DOI=10.1016/0167-4781(94)90018-3;
                                                                                  SEQUENCE FROM N.A.
PubMed=11054574; DOI=10.1016/S0378-1119(00)00382-6;
PubMed=11054574; DOI=10.1016/S0378-1119(00)00382-6;
PubMed=11054574; DOI=10.1016/S0378-1119(00)00382-6;
MOSS P., Paeper B., Wang M., Argonza-Barrett R., Lei H., McCuaig J.,
MOSS P., Paeper B., Wang M., Argonza-Barrett B., Wang M., Argonza-Barrett B., Wang M., Argonza-Barrett B., Wang M., Argonza-Barrett B., Wang M., Argonza-Barrett B., Wang M., Argonza-Barrett B., Wang M., Argonza-Barrett B., Wang M., Argonza-Barrett B., Wang M., Argonza-Barrett B., Wang M., Argonza-Barrett B., Wang M., Argonza-Barrett B., Wang M., Argonza-Barrett B., Wang M., Argonza-Barrett B., Wang M., Argonza-Barrett B., Wang M., Argonza-Barrett B., Wang M., Argonza-Barrett B., Wang M., Argonza-Barrett B., Wang M., Argonza-Barrett B., Wang M., Argonza-Barrett B., Wang M., Argonza-Barrett B., Wang M., Argonza-Barrett B., Wang M., Argonza-Barrett B., Wang M., Argonza-Barrett B., Wang M., Argonza-Barrett B., Wang M., Argonza-Barrett B., Wang M., Argonza-Barrett B., Wang M., Argonza-Barrett B., Wang M., Argonza-Barrett B., Wang M., Argonza-Barrett B., Wang M., Argonza-Barrett B., Wang M., Argonza-Barrett B., Wang M., Argonza-Barrett B., Wang M., Argonza-Barrett B., Wang M., Argonza-Barrett B., Wang M., Argonza-Barrett B., Wang M., Argonza-Barrett B., Wang M., Argonza-Barrett B., Wang M., Argonza-Barrett B., Wang M., Argonza-Barrett B., Wang M., Argonza-Barrett B., Wang M., Argonza-Barrett B., Wang M., Argonza-Barrett B., Wang M., Argonza-Barrett B., Wang M., Argonza-Barrett B., Wang M., Argonza-Barrett B., Wang M., Argonza-Barrett B., Wang M., Argonza-Barrett B., Wang M., Argonza-Barrett B., Wang M., Argonza-Barrett B., Wang M., Argonza-Barrett B., Wang M., Argonza-Barrett B., Wang M., Argonza-Barrett B., Wang M., Argonza-Barrett B., Wang M., Argonza-Barrett B., Wang M., Argonza-Barrett B., Wang M., Argonza-Barrett B., Wang M., Argonza-Barrett B., Wang M., Argonza-Barrett B., Wang M., Argonza-Barrett B., Wang M., Argonza-Barrett B., Wang M., Argonza-Barrett B., Wang M., Argo
                                                                                                                                                                                                                                                                                                                                  Dihanich M.E., Spiess M.; "A novel serine proteinase-like sequence from human brain."; Biochim. Biophys. Acta 1218:225-228(1994).
"Molecular cloning of the human kallikrein 15 gene (KLK15).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genew; HGNC:20453; KLKIS.

GO; GO:0005576; C:sextracellular; NAS.

GO; GO:0004252; F:serine-type endopeptidase activity; NAS.

GO; GO:0006508; P:proteolysis and peptidolysis; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                       PUDMed=14759258; DOT=10.1186/gb-2004-5-2-r8;
Hillman R.T., Green R.E., Bremner S.E.,
"An unappreciated role for RNA surveillance.";
Genome Biol. 5:RESEARCHO08.1-RESEARCHO08.16(2004).
-! FUNCTION: Procease whose physiological substrate is subcELLULAR LOCATION. Secreted (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=Q9H2R5-3; Sequence=VSP_005406, VSP_005407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Event=Alternative splicing; Named isoforms=4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=1;
IsoId=Q9H2R5-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PEAM; PRO0089; Trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp SPc; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN HIS; 1.
                                                                                                                                                                                                                                                                     PRELIMINARY PARTIAL SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR009003; Pept Ser Cys.
InterPro; IPR001254; PeptIdase 81.
InterPro; IPR001314; Peptidase_SIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X75363; CAA53145.1; ALT_SEQ.
HSSP; P00760; 1EZX.
MEROPS; S01.081;
                     regulation in prostate cancer."; J. Biol. Chem. 276:53-61(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF242195; AAG09469.1; -. EMBL; AF242195; AAG09470.1; -. EMBL; AF242195; AAG09471.1; -. EMBL; AF241395; AAG09472.1; -. EMBL; AF243527; AAG033354.1; -.
                                                                                                                                                                                                                        Gene 257:119-130(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       subfamily
                                                                                                                                                                                                                                                                                            TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=4;
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63 CSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLRLPVRVTS 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 SVOPLPLPNDCATAGTECHVSGWGITNH-----PRN--PFPDLLQCLNLSIVSHATC 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 IFLLLCVLGLSQAAT -- PKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Brain;
MEDLINE=20525460; PubMed=11072088; DOI=10.1016/S0167-4781(00)00206-2;
Mitsui S., Okui A., Kominami K., Uemura H., Yamagushi N.;
Mitsui S., Othing and tissue-specific splicing variants of mouse
hippostasin/TLSP (PRSS20).";
                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                Charge relay system (By similarity)
Charge relay system (By similarity)
Charge relay system (By similarity)
N-linked (GloNAC. .) (Potential).
N-linked (GloNAC. .) (Potential).
                                                                                                                                                                                                                                                                                                               SHNEPGTAGSPRSO -> PLSSP (in Ref. 2)
Alternative splicing; Glycoprotein; Hydrolase; Serine protease;
                                                                                                                                                                                                                                                                                                                                                                                                           16;
                                                   (Potential)
                                                                                                                                                                                                                                                                                                                                                                      43.6%; Score 599; DB 1; Length 256; 47.1%; Pred. No. 4.2e-40;
                                                                                                                                                                                                                                                                                                                                                                                                         88; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUB=Brain;
Yamaquothi N.,
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
!- SIMILARITY: Belongs to peptidase family S1.
                                                                                                                                                                                                                                                                                                                                   B5EBF8D6022786B5 CRC64;
                                                                                                                                                                                                        Missing (In isoform 2).
/FIId=VSP 005405.
V -> G (in isoform 3).
/FIId=VSP 005406.
Missing (In isoform 3).
                                                                                                                                                                       Missing (in isoform 4). /FTId=VSP 005404.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                               Activation peptide (P
Kallikrein 15.
Charge relay system (
Charge relay system (
                                                                                                                                                                                                                                                                                              /FTId=VSP_005407.
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                                                                                                                                                                                                                                                                                                                                                                                                       32; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 47.13
Matches 121; Conservative
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                                                                                                                                                                                                                                                                                 162
                Signal; Zymogen.
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237
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
05-077-2004 (TrEMBLrel. 28, Last annotation update)
25-077-2004 (TrEMBLrel. 28, Last annotation update)
Hippostasin prostate type (Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310015108 product:protease, serine, 20, full insert sequence) (Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310040F07
product:protease, serine, 20, full insert sequence).
Name=2310015108Rik;
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MEDLINE=20525460; PubMed=11072088; DOI=10.1016/S0167-4781(00)00206-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                              5;
                                                                                                                                                                                                                                                                                                                                       DB 2; Length 249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mitsui S., Okui A., Kominami K., Uemura H., Yamagushi N.; "cDNA cloning and tissue-specific splicing variants of mouse hippostasin/TLSP (PRSS20)."; Biochim. Biophys. Acta 1494:206-210(2000).
                                                                                                                                                                                                                                                                                                                                                                              95; Indels
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Yamaguchi N., Mitsui S.;
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
[3]
                                                                                                                                               .4e-40;
                HSSP; P00760; 1EZX.
MEROPS; S01.257; -.
MGD; MGI:1929977; 2310015108Rik.
GO; GO:0005615; C:extracellular space; TAS.
                                                                                                                                                                                                                                                                                                                                                                        33; Mismatches
                                                                                                                                                                                                                                                                                                                                     43.5%; Score 597.5; 47.0%; Pred. No. 5.4
                                                                                            InterPro; IPR001254; Peptidase SI.
InterPro; IPR001314; Peptidase SIA.
InterPro; IPR009003; Pept_Ser_Cys.
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STRAIN=CS7BL/6J; TISSUE=Tongue;
STRAIN=CS7BL/6J; TISSUE=Tongue;
STRAIN=CS7BL/6J; TISSUE=Tongue;
Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Sumi N., Ishii Y., Nakamura S., Ikegami T., Kashiwagi K., A Yamamoto R., Inoue K., Tozawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Xoneda Y., Ishikawa T., Ozawa K., Tanaka T., Hayshizaki Y., Tanamatsu Y., Rikin integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the RIKEN Genome Exploration Research Group Phase I & II Team, "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
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STRANIE-CS7BL/G0; TISSUB=Tongue;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Whormalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
STRAIN=C57BL/6J; TISSUE=Tongue;
MEDLINE=9957923; Pubmed=1034636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.,
"High-efficiency full-length cDNA cloning.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=CS7BL/6J; TISSUE=Tongue;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
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MGD; MGI:1929977; 2310015108Rik.
GO; GO:0005615; C:extracellular space; TAS.
InterPro; IPR001254; Peptidase S1.
InterPro; IPR001314; Peptidase S1.
InterPro; IPR0931314; Peptidase S1.
InterPro; IPR093031; Peptidase S1.
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Tongue;
The FANTOM Consortium,
                                                                                                                               Meth. Enzymol. 303:19-44(1999).
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STRAIN-CS7BL/6J; TISSUE=Tongue;
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PRINTS, PR00722, CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPc, 1.
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61 AHCSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGA--STSHEHDLRLLRLRLPV 118
                                                                                                                                                                                                                                                                                              147 FFTRAVQPLTLSPHCVAAGTSCLISGWGTTSSPQLRLPHSLRCANVSIIEHKECEKAYPG 206
                                                                                                                                                                                                                                                                                                                                          119 RVTSSVQPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPG 178
                                                                                                                                                                           28 MILKLIALALVTGHVGGET-RIIKGYECRPHSQPWQVALFQKTRLLCGATLIAPKWLLTA 86
                                                                                                                                                        1 MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTA 60
                                                                                                                         5; Gaps
                                                                                         Query Match 43.5%; Score 597.5; DB 2; Length 276; Best Local Similarity 47.0%; Pred. No. 6e-40; Matches 118; Conservative 33; Mismatches 95; Indels 5;
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; UNKNOWN_1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolae; Protease; Serine protease.
SEQUENCE 276 AA; 30753 MW; 90BDC03A8ABI78D6 CRC64;
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266 FNWIHEVMRNN 276
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